

[x1] SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGGCACCG GTAGTTTGAA CCAAAAGGCAC AATCGAGCGG CAAACGAACG GAAGACACACA	60
ACCATGAAGA TGCTGAAATC GATCGCGGCA GGTCTGACCG CCGCGGCTGC AATCGGGCGCC	120
GCTCGGGCCG GTGTGACTTC GATCATGGCT GCGGCGCCGG TCGTATACCA GATGCAACCG	180
GTCTCTTCG GCGCGGCACT GCGTTCGAC CCGGCATCCG CCCCTGACGT CCCGACCGCC	240
GCCCCAGTTGA CCAGCCTGCT CAACAGCCTC GCGCATCCCA ACGTGTCTTT TCGGACCAAG	300
GGCACTCTTG TCGAGGCGCG CATCGGGGCG ACCGAGCGCG GCATCGCGCA CCACAGCTTG	360
AAGAAGGCGG CCGAGCGCGG GGATCTGCGG CTGTGCTTCA GCGTGACCAA CATCGAGCGG	420
GCGGCGCGCG GTTCGGCCAC CCGCAGCTT TCGCTCTCGG GTCCGAGGCT CTCGTGCGCG	480
GTCACGCAGA ACCTCAGCTT CGTGAATCAA GCGGCTGGA TCGTGTACCG CGCATCGCGG	540
ATGGAGTTGC TCGAGGCGCG AGGGNAACTG ATTGGCGGGC CGGTTTCAGC CCGCTCTTCA	600
GCTACGCGCG CCGCTTGGTG ACGCTTCCTT CTCGAACACT CCGCGCTGTA GCACGGTGGG	660
GTNTCCGCAG GCGCGCAGCG ACCGCGCGGT GCAAGCGCTC CTCGAGTAG GTGGTGNCTC	720
GNCACCAAGG ANCAACCCCN NNTCGMCMNT TCTCGMCMNT GNATGA	766

[2] INFORMATION FOR SEQ ID NO:2:

[1] SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

[x1] SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCATCACC ATCACCATCA CGATGAAGTC ACGGTAGAGA CGAAGTCGCT CTTCCCGCCA	60
GACTTCCTCA GCGAGCTGGA CGCTCTGCG CAAGCGGTA CCGAGAGCGC GGTCTCGGG	120
CTGGAAGGGU TCCCGCGGG CTCGGCTTG CTGGTASTCA AACGAGGCTC CAACGCGGG	180
TCCCGGTTCC TACTCGACCA AGCCATCAGC TCGGCTGCTC GGCATCCCGA CAGCGACATA	240

TTTCTGAGCG	ACGTGACCGT	GAGCCGTCGG	CATGCTGAAT	TCCGATTGGA	AAACACCGAA	300
TTCAATGTGG	TGGATGTGGG	GAGTCTCAAC	GGCACCTACG	TCAACCGCGA	GCLUGTGGAAT	360
TGGGGGGTGG	TGGCGAACGG	CGACGAGGTC	CAGATCGGCA	AGCTCCGGTT	GATGTTCCTTG	420
ACCGGACCCA	AGCAAGGCGA	GGATGACGGG	AGTACCGGGG	GCCCGTGAGC	GCACCGGATA	480
GCCCCGGCGT	GGCCGGGATG	TCCATCGGGG	CGGTCTCTCG	ACCTGCTACG	ACCGGATTTT	540
CCCTGATGTC	CACCATCTCC	AAGATTCGAT	TCTTGGGAGG	CTTGAGGCTC	GGGTGACCC	600
CCCCGCGGGC	CTCATTCTGG	GCTTCGGGCG	GGTTTCACCC	CTTACCNACT	GGCNCCTGGG	660
TTCGCAATTC	NTTCTTCTCT	GGCCGMAAAG	GGACCTTTAN	CTTCCCGCTN	GAAAGGCTNA	720
TCCNGGGCCC	NTCCTNGAAN	CCCTNTCCCC	CT			752

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 813 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCATC	ACCATCACCA	TCACACTTCT	AACGCGCCAG	CGGCTCGGGG	GGGTGAGGCA	60
CCACGCGACA	CCGGGCCCCG	TCGATCTGCT	AGCTTGAGTC	TGGTCAGGCA	TGGTCTTCAG	120
CAGCGCGATG	CCCTATGTTT	GTGCTGAGCT	CAGATATCGC	GGCAATCCAA	TCTCCCGCCT	180
GCGGCCGGCG	GTGCTGCAAA	CTACTCCCGG	AGGAATTTCC	ACGTGCGCAT	CBAGATCTTC	240
ATGCTGGTCA	CGGCTGTGCT	TTTGCTCTGT	TGTTGCGGTC	TGGCCACGGC	CGCGCCCAAG	300
ACCTACTGCG	AGGAGTTGAA	AGGCACCGAT	ACCGGCCAGG	CGTGCCAGAT	TCAAATGTCC	360
GACCCGGGCT	ACAACATCAA	CATCAGCCTC	CCAGTTACT	ACCCCGACCA	GAGTCTGCTG	420
GAAAATTACA	TGGCCGAGAC	GGCCGACAAG	TTCTCTAGCG	CGGCCACATC	GTCCACTCCA	480
CCGGAAGCCC	CCTACGAATT	GAATATCACC	TGCGCCACAT	ACCACTCCGC	GATACCGCCG	540
CGTGGTACCG	AGGCCGTGGT	CTTCAGGCTC	TACCAGAAAG	CGGGCGGGCA	GCADCCAAAG	600
ACCACGTACA	AGGCCTTCGA	TTGGGACCCG	GCCTATCGCA	AGCCAATCAC	CTATGACACG	660
CTGTGCGAGG	CTGACACCGA	TCCGCTGCCA	GTGCTCTTCC	CCATTGTTGC	AAGTGGAGCT	720

GAGCAACCCA GACCGGGACA ACWGGTATCG ATAGCCGCCN AATGCCGGGT TGGAAACCCWG 780
 TGAAATATC ACAACTTCGC ATCACAATAA NAA 813

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATGAAC ACGGCCGCGT CCGATAACTT UCAGCTGTCC CAGGGTGGGC AGCGATTCCG 60
 CATTCGATC GGGCAGGCGA TGGCGATCGC GGGCCAGATC CGATCGGGTG GGGGGTCACC 120
 CACCGTTCAT ATCGGGCCTA CCGCCTTCCT CGCCTTGGGT GTTGTCCACA ACAACGGCAA 180
 CCGCGCACGA GTCCAACGCG TGATCGGGAG CGCTCCGCGG GCAATCTCG GCATCTCCAC 240
 CCGCGACGTG ATCACCAGCG TCGACGGCGC TCCGATCAAC TCGGCCACCG CGATGGCGGA 300
 CGCGCTTAAC GGGCATCATC CCGGTGACGT CATCTCGGTG AACTGGCAAA CCAACTCGGG 360
 CCGCACCCGT ACAGGGAAAG TGACATTCGC CGAGGGACCC CCGGCTCAT TTCGTGGYGG 420
 ATACCACGCG CCGGCCGGCC AATTGCA 447

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 604 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCCACTGC GGTCCGCGAG TATGTGCGCC AGCAAAATGTC TGGCAGCCGC CCAACGGAAT 60
 CCGGTGATCC GACGTCCAG GTTGTGGAAC CCGCCGCCGC GGAATATCG GTCCATGCGT 120
 AGCCCGGCGA CGGCGAGCGC CGGATGGCG CCACTGAGGA GGTGGGCAAT TTGGCGGGGC 180

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COGSCGACCG NGAGCGCCCG AATGCGCCGA GTGAGGAGGT GGCAGTCAT GCCCAGNCTG 240
ATCCAATCAA CCTGNATTCG GNCNGGCGN CCATTGACA ATCGAGGTAG TGACCCCAAA 300
TGAATGATCG AAAACGGGNG GNCACCTCCG NTGTTCTGGT CCTGNTAGGT GNCNGNCTCG 360
NCTNGGCGNY ATCAGGATGT TCTTCGNCGA AANCTGATGN CGAGGAACAG GGTGTNCCCG 420
NNANCCNAN GGNSTCCNAN CCGNNNTCC TCGNCGANAT CANANAGNCG STTGATNGA 480
NAAAAGGCTG GANCAGNNNN AANTNGNGGN CCAANAANC NNANNGGNG NNAGNTGNT 540
NNNTNTTNNC AANNNNNTG NNGMNGMNCN NNNCAANCNN NTHNNNGNAA NNGGNTTNTT 600
EAAT 604

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(2) INFORMATION FOR SEQ ID NO:6:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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TTGCANGTCG AACCACTCA CTAAAGGGAA CAAAAGCTNG AGCTCCACCG CGGTGCGGGC 60
CGCTCTAGAA CTAGTGKATH YYCKGGCTG CAGGAATYCG GYACGAGCAT TAGGACAGTC 120
TAACGGTCCY GTTACGGTGA TCGAATGACC GACGACATCC TGCTGATCGA CACCGACGAA 180
CGGGTCCGAA CCTCACCCT CACCCGGCG CAGTCCCGYA ACGCGCTCTC GCGGCGGCTA 240
CGGGATCGGY TTTTCGGGY GTTGGYCGAC GCGGAGGYCG ACGACGACAT CGACCTCGTC 300
ATCCTCACCG GYCCCATCC GGTGTTCTGC GCGGACTCG ACCTCAAGGT AGCTGGCCGG 360
GCAGACCGCG CTCCCGGACA TCTCAGCGG GTGGGCGGCC ATGACCAAGC CGGTGATCGG 420
CGGATCAAC GCGCCGCGG TCACCGGCGG GCTCGACTG GCGCTGTACT GCGACRTCT 480
GATCGGCTCC GAGCAGCGCG GTTCGNCGA CACCCAGCCC CGGGTGGGCG TGCTGCCCAC 540
CTGGGGACTC AGTGTGTCT TGGCGCAAAA GGTGCGCAAT GCGCTGGGCG GCTGATGAG 600
CCTGACCGGC GACTACCTGT CCGTGACCGA GGC 633

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(2) INFORMATION FOR SEQ ID NO:7:

- (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(=1) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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CGACGACGAC GGGCGCGGAG AGCGGGCGCG AACGGCGATC GACGCGGCCC TGGCCAGAGT    60
CGGCAACCAAC CAGGAGGGAG TCGAATCATG AATTTGTCA ACCATATTGA GCGCGTCGCG    120
CCCCGCGGAG CCGGCGGCGC GGTGCGCGAG GTCTATGCGG AGGCGCGCGG CGAGTTCGSC    180
CAGCTGCGCG AGCGGCTCGC CATGCTGTTC CCGGACGAGG GACTGCTCAC CCGCGGCTGG    240
GCGAGGTTTC GCGAGACACT GTTGTGCGGC CAGGTGCGGC GTGGCGGCAA GGAAGCGGTC    300
GCGCGCGCGG TCGCGGCGAG CCTCGGCTGC CCTTGGTGGC TCGACGACA CACCAACATG    360
CTGTACGCGG CAGGCGCAAC CGACACGCGC GCGGCGATCT TGGCGCGCAC AGCAGCTGCC    420
GCGGCTGACC CGAAGCGGCG GTATGTGCGG TGGCGCGCAG GAACCGGAC ACCGCGCGGA    480
CGCGCGGCGC CGTTGCGGCG GGATGTGCGC GCGGAATACC TGGGCGGCGC GTTGCAATTC    540
CACTTCATCG CAGCGCTGGT CCTGCTGCTG CTGCGAGAAA CCTTCTGCGC GCGGCGGCGG    600
CGCGCGCAAC AGCTCATGCG CCGCGCGGCT GAGCTGCTGT TCGCGCGCAA GGTGCGCGCG    660
GAGCATCGCG CCGGCGGCTC CACCGCGCGG CTCGAGCGGC GAACGCTGCC CGACGATCTG    720
GCATCGGCAA CACCGTCCGA GCGCATAGCA ACGCGCTTCG CCGCGCTCGG CCACCACTCG    780
GACACCGCGC CGCACCTGCC GCGACCGACT CGTCAGGTGG TCAGCGGCTT CGTGGGCTCG    840
TGGCAGCGCG AGCCAATGCC GATGAGCAGT CGCTGCGCGA ACGAGCACAC CCGCGAGCTG    900
CGCGCGGACC TCGACGCGCG CACCGCTCTT GCGCTGCTGA CCGGCGTGGC CCGCGATCAG    960
GTGAGCGAGG ACGACGTGCG CGCGGCGCGA TCGTGTCTCG ACACCGATCG GCGCTGCTTT    1020
GCGCGCGCTG CCGGCGGCGC CTTACCGCGC GCGCGGCGCA TCGGCGCTCG GATCGCGCGC    1080
GCGCGCGGAG GCGAGGTCTC CCGGCAAAAC CCGACTGGGT GAGTGTGCGC GCGCTGCTCG    1140
TAGGCTGTCA TCGCTGCGCG GAGGATCTC GCGGCGGCGA ACGGAGGTTC CGACACAGGT    1200
GGAAGCTGCG CCGACTGGCT TCGCGCGCAA CCGCGTCTGT GCGCTTGGCT TCGCGGCACT    1260
GCGCGATCAG GTGCGCGCGC GCGCTTGGCT GAGGCTCCAG CTCAGCTGCG CGTACCGGAA    1320

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GGACCGGAGG GTCAACGGGG GTCAACCTGC GCGCCCAAGG AA 1362

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGACGALXC	CGATATGCCG	GGCACCCTAG	CGAAGGCCGT	CGCCGACCCA	CTCGGGCGCG	60
GTATCGCTCC	CGTTGAGGAC	ATTCAAGACT	GCTTGGAGGC	CGGCTTGGGG	GAAGCCGGTC	120
TGATGACGT	CGCCCGTGT	TACATCATCT	ACCGGAGCG	CGCGGCGGAG	CTCGGACCG	180
CTAAGGCCTT	GCTCGGCGTG	CGGACCGACT	TAAAGCTGAG	CTTGGCGGCC	GTGACGGTAC	240
TGCGCGAGCG	CTATCTGCTG	CACGACGAGC	AGGCGCGGCC	GGCGGAGTCG	ACCGGCGGAGC	300
TGATGGAGCG	ATCGCGCGCG	TGTGTGCGCG	CGGCGGAGCA	CCAGTATGAG	CCGGGCTCGT	360
CGAGGCGGTC	GGCCGAGCGG	TTCGCCACCG	TATTACGCAA	CGTGGGATTC	CTGCCGAATT	420
CGCCGACGTT	GATGAAGCTT	GGCACCAGCG	TGGGACTGCT	CGCCGGCTGT	TTTGTTCCTG	480
CGATTGAGGA	TTCGCTGCAA	TGGATCTTTG	CGACGCTGGG	ACAGGCGGCG	GAGCTGCGAGC	540
GGGCTGGAGG	CGGCACCGGA	TATGCGTTCA	GCCACCTGCG	ACCGGCGGCG	GATCGGGTGG	600
CGTCGACGCG	CGGCACGCGC	AGCGGACCGG	TGTGCTTTCT	ACGGCTGTAT	GACAGTGCCG	660
CGGCTGTGCT	CTCCATGGGC	GCTCGCCGCG	GTGCGCGCTG	TATGGCTGTG	CTTGATGTGT	720
CGCACCAGGA	TATCTGTGAT	TTCGTCACCG	CCAAGGCCGA	ATCCCGCAGC	GAGCTCCCGC	780
ATTTCAAGCT	ATCGTTTGGT	GTGACCGAGC	CGTTCTTGCG	GGCGGTGAGG	CGCAACGGCC	840
TACACCGGCT	GCTCAATCGG	CGAACCAGCA	AGATCGTGGC	GCGGATGCCC	GCCCGCGAGC	900
TGTTGAGGTC	CATCTGCAAA	GCGCGGCGAG	CGGTTGGCGA	TCCCGGGCTG	GTGTTTCTCG	960
ACACGATCAA	TAGGCTTAAC	CGGTTGCGCG	GGAGAGGCGG	CATCGAGGCG	ACCAACCCGT	1020
GCGGCGAGGT	CCACTGCTTG	CCTTAGGAGT	CATGTAAATCT	CGGCTCGATC	AACCTCGCCC	1080
GGATGCTGCG	CGACGCTGCG	GTGAGCTGGG	ACCGGCTCGA	GGAGGTGCGC	GCTGTGGCGG	1140
TGCGGTTGCT	TGATGACGTC	ATCGATGTCA	GCGGCTAGCC	CTTCCCGGAA	CTGGGTGAGG	1200

CGGCCCCCGG CACCCGCAAG ATCGGGCTGG GAGTCATGGG TTTGGCGGAA CTGCTTGCCG	1260
CACTGGGTAT TCCGTACGAC AGTGAAGAAG CCGTCGGTT AGCCAGCCGG CTCATGCGTC	1320
GCATACAGCA GCGGCGGAC ACCGCATGCG GAGGCGTGGC CGAAGAGCGG GCGGCATTCC	1380
CGGCGTTGAC CGATAGCGG TTCGCGCGGT CGGCGCCGAG GCGCAACGCA CAGGTCACCT	1440
CGGTGCTCC GACGGGCA	1458

(2) INFORMATION FOR SEQ ID NO:9:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCTGTAAAT CGTGCTGGAT CTGGAACCGC GTGGCCCGCT ACCTACCGAG ATCTACTGSC	60
GGGCGAGGGG GCTGGCCCTG GGCATGCGG TCGTCGTAGT CGGGATCGCG GTGGCCATCG	120
TCATCGCCTT CGTCGACAGC AGCGCCGCTG CGAAACCGGT CAGCGCCGAC AAGCCGCGCT	180
CGGCGGAGAG CCATCCGCGC TCGCGGCGAC CCCAAGCACC CCAGCCCGCC GCGCAAACCG	240
AAGGTAACGC CGCCGCGGCG CGGCGCGAGG GCGAAGACC CGAGACACC ACGCCAGCGG	300
CGCGGTGCA GCGCGCGCG GTGCTCAAGG AAGGCGACGA TTGCGCGAT TCGACGCTGG	360
CGGTCAAAGG TTGACCAAC GCGCCGCGT ACTACGTCG CGACCGCGG AACTTCACCA	420
TGGTGGTCAC CAACATCGGC CTGGTGTCT GTAAACGCA CATTGAGGCG GCGGTGTTGG	480
CGCGCTACCT TTAATCGCTG GACAAACAAC GGTGTGCTG CAAGCTGGAC TCGCGCGCGT	540
CGAATGAGAC GCTGCTCAAG ACCTTTTCCC CGGTCAGCA GTTAACGACC GCGGTGACT	600
GGACCGGAT GCGATCGCG CGCGGCTGCC CATCGCGCG GCGGCGGATC GCGCGCGGCA	660
CCTACAACTT CGTGGTACAA CTGGGCAATC TCGGCTCGCT GCGGTTCCG TTCATCTGA	720
ATCAGCGCGG GCGCGCGCG GCGCGGTAC CGGCTCGGG TCGAGCGGAG GCGGCTCGSC	780
CGGASTCTCC GCGCAAGGC GGATATTTAT TGATCGCTGA TGCTCGATT CCGCAGCTGT	840
GACAACCCCT CGCTCGTGC CG	862

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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TTGATCAGCA CCGGCAAGGC CTCACATGCC TCCCTGGGTC TGCAGGTGAC CAATGACAAA      60
GACACCCCGG GCGCCAGCAT CGTCCAAGTA GTGGCCGGTC GTGCTGGCGC GAACGCTGGA      120
GTGCGGAAGG GCGTCCTTCT CACCAAGCTC GAGGACCGCC CGATCAACAG CGCGGACGGC      180
TTGTTTCCCG CCGTCCGGTC CAAAGCGCCG GCGCCGACGG TGGCGCTAAC CTTTCAGGAT      240
CCCTCGGGCG GTAGCCGCGC AGTCCAGCTC ACCCTCGGCA AGGCGGAGCA GTGATGAAGG      300
TCGCGCGCCA GTCTTCAAGG CTCGGATATA CGGTGGCACC CATGGAACAG CTTGCGGAGT      360
TGGTGGTTGG CCGGCACTT GTGCTGCTCG TTGACGATCG CACGGCGGAC GGCGATGAAG      420
ACCACAGCGG GCGGCTTGTC ACCGAGCTGC TCACCGAGGC CGGCTTTGTT GTCGACGGCG      480
TGCTGCGGCT GTCGGCGGAC GAGGTGAGAA TCCGAAATGC GCTGAACACA GCGGTGATCG      540
GCGGGCTGGA CTTGCTGCTG TCGGTCGGCG GCGCCGCGGT GACGCTGCGC GATGTCACCC      600
CGGAAGGAC CCGGACATT CT                                     622

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(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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GGGCGAGCGG TAAGCTGTT GCGCGCGGAC ACGTGGTGT TGACAGCATG CCGCGGTGGC      60
ACCAACAGCT CGTCTCAGG CGCAGGCGGA AGTCTGGGT CCGTCACTG CCGCGCGAAG      120
AAGGAGCTCG ACTCCAGCG CTCGACCGCA CAGAAAATG CCGTGCAGCA GTTCTCTAT      180

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GCCTACGTGC GATCGTGCNC GGCTACACG TTGGACTACA ACCCCAACGG GTCCGCTGCC 240
GGGCTGACCC AGTTTCTCAA CACGAAACCC GATTTGCCCC GCTCGGATGT CCGCTTGAAT 300
CCGTCGACCG GTCAACCTGA CCGGTCGCCG GAGCGGTCCG GTTCCCCGGC ATGGGACCTG 360
CCGACGGTGT TCGGCCCGAT CGCGATCACG TACAATATCA AGGGCGTGAG CACGCTGAAT 420
CTTGACGGAC CCACTACCGC CAAGATTTTC AACGGCACCA TCACCGTGTG GAATGATCCA 480
CAGATCCAAG CCGTCACCTC GGGCAGCGAC CTGCCGCCAA CACCGATTAG CGTTATCTTC 540
CGCAGCGACA AGTCCGGTAC GTCGGACAAC TTCCAGAAAT ACCTCGACCG TGTATCCAAC 600
GGGCGCTGCG GCAAAGGGCG CAGCGAACC TTCAGCGGGC GCTCGCGCT CGGCGCCAGC 660
GGGAACACG GAACGTCCGC CCACTGCGG AGGACCGAG GGTGATCAC CTACACCGAG 720
TGCTCCTTTC CGGTGGGTAA GCACTTGAAC ATGGCCGAGA TCATCACGTC GCGGGGTCCG 780
GATCCAGTGG CGATCACCAC CGAGTCGCTC GTTAGACAA TCDCCGGGGC CAAGATCATG 840
GGACAAGGCA ACGACCTGGT ATTGGACAG TCGTCGTTCT ACAGACECAC CCAGCCTGGC 900
TCTTACCCGA TCGTGCTGGC GACCTATGAG ATCGTCTGCT CGAATACCC GGATGCGAGC 960
ACCGSTACTG CGTAAGGGC GTTATGCCAA GCGCGATTG GTCCAGCCCA AGAAGGCTG 1020
GACCAATAGC GCTCCATTCC GTTCCCCAA TCCTTCCAG CAAAATTGGC GGCGCGGTG 1080
AATGCTATTT CTGACCTAG TGAAGGGAAT TCGACGCTGA GCGATGCCGT TCGGCACTA 1140
GGGTCCCAAT TTGGGCGCTA TCAGCTATTG CGGCTGCTGC GCGAGGCGG GATGGGCGAG 1200

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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GCAGCGAGCT GCAGTCCGTG CTGTTGACG AACTGGGAT GCUGAAGACC AAACGCACCA 60
AGACCGGCTA CACCACGGAT GCGACGCGC TGCAGTCGTT GTTCGACAAG ACCGGGCGTC 120
CGTTTCTGCA ACATCTGCTC GCGCACGCG ACCTCACCG GCTCAGGTC ACCGTCGAGC 180

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GGTTGCTCCA AGCGGTGGCC GCGGACGGCC GCATCCACAC CACGTTCAAC CAGACGATCG      240
CCGCGACCGG CCGGCTCTCC TCGACCGAAC CCAACCTGCA GAACATCCCG ATCGGCACCG      300
ACCGGGGCGG GCGGATCCCG CACCGCTTCG TGCTCGGGGA CGGTTACGCG GAGTTGATCA      360
CGGCGGACTA CAGCCAGATC GAGATCGGGA TCATGGGGCA CCTGTCCCGG GACGAGGGCC      420
TCATCGAGGC GTTCAACACC GGGGAGGACC TGTATTGGTT CGTGGCGTCC CGGCTGTTCG      480
GTGTGCCCAT CGACGAGGTC ACCGGCGAGT TGCGGCGCCG GGTCAAGGCG ATGTCTTACG      540
GGCTGGTTTA CGGGTTSAGC GCTTACGGCC TGTCGCAGCA GTTGAAATC TCCACCGAGG      600
AAGCCAAACG GCAGATGGAC GGTATTTCG CCGGATTCGG CGGGGTGGCG GACTACCTGC      660
GGCGCTTACT CGAGCGGGCC GCGAAGGCG GGTACACCTC GACGCTGCTG GCGCGTGGCC      720
GTTAAGTGGC CGAGCTGGAC AGCAGCAACC GTCAAGTCCG GGAGCCCGCC GAGCGGGGCG      780
CGCTGAGCGC GCCATCCAG GCGAGCGCGG CCGACATCAT CAAGGTGGCC ATGATCCAGG      840
TGGACAAGGC GCTCAACGAG GCACAGCTGG CGTCGCCCAT GCTGCTGAG GTCCACGACG      900
AGCTGCTGTT CGAAATCGCC CCGGTGAAC GCGAGCGGGT CGAGGCTCTG GTGCGGAGCA      960
AGATGGGCGG CGCTTACCGC CTCGACGTCC CGCTGGAGGT GTCGCTGGCC TACGCGCCCA      1020
GCTGGGACCC GCGGCGGAC TGAGTCCGA GGTGTCATCT GGGCGGGAA TTGGGCGATT      1080
TTTCCGCGCT GAGTTCACGC TCGCGCAAT CGGACCGAG TTTGTCCAGC GTGTACCGT      1140
CGAGTAGCCT CGTCA                                     1155

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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GAGCGCGGTC TGCTGTTTGA ACGGTTTAC CGTGGGCAT CCGCAGGGG GTTGCCGGGT      60
TCGGGCTTCG GGTGGGCAI CGTCAGACAG GTGCTGCTCA ACCAGGGCGG ATTGCTGGCG      120
ATCGAAGACA CCGACCCAGG CGGCCAGCCC CCGGAAAGCT CGATTACGT GCTGCTCCCC      180

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GGCCGTCGGA	TGCCGATTC	GCAGCTTCCC	GGTGGGACCG	CTGGCBCTCG	GAGCAGCGAC	240
ATCGAGAACT	CTCGGGGTTT	GGCGAAGGTT	ATCTCAGTGG	AATCTCACTC	CADCGCGCA	300
ACCTACTTST	GCAGTTACTG	TTGAAAGCCA	CAGCCATGCC	AGTCCAGCCA	TGCCCCAGTT	360
GGCCCCAGTA	GTGGGCTTAG	TACAGGAGAA	GCAACUTAGC	GACATGACGA	ATCAGCCAGC	420
GTATTGCGCA	CGCGCCGAGC	AGCCGGGAAC	CCAGGTTTAT	GCTCAGGGGC	AGCAGCAAAC	480
GTACAGCCAG	CAGTTGCACT	GGCGTTACCC	ACCGTCCCGG	CCCCCGCAGC	CAACCCAGTA	540
CCGTCAACCC	TACGAGGCGT	TGGGTGGTAC	CGGGCGGGGT	CTGATACCTG	GCGTGATTCC	600
GACCATGAGC	CCCCCTCCTG	GGATGGTTCC	CCAGCGCCCT	GCTGCAGGCA	TGTTGGGCAT	660
CGGCGCBCTG	ACGATAGCGG	TGCTGTCCGC	CGGCATCCGC	GGCGCGGGCG	CATCCCTGGT	720
CGGGTTCAAC	CGGGCAGCCG	CGGGCCCCAG	CGGCGGCTCA	GTGGCTGCCA	GCGGGGCGCC	780
AAGCATCCCC	GCAGCAACA	TGCGGCGGGG	GTGCGTGGAA	CAGGTGGCGG	CCAGGTTGGT	840
GCCAGTCTC	GTCTATTGG	AAACCGATCT	GGCGCGCCAG	TGGGAGGAGG	GCTCCCGCAT	900
CATTCTGTCT	GCCGAGGGGC	TGATCTTGAC	CAACAACCCAC	GTGATGCGCG	CGGCGGCGCA	960
GCTTCCTCTG	GGCAGTCCGC	CGCGGAAAGC	GACGCTAACG	TTCTCTGAGG	GGCGGACCGC	1020
ACCTTTCAAG	GTGGTGGGGG	CTGACCCGAC	CAGTGATATC	GCGGTGCTCC	GTGTTCAAGG	1080
CGTCTCCGGG	CTCAGCCCGA	TCTCCCTGGG	TTCTCTCTCG	GACCTGAGGG	TGGGTCAGCC	1140
GGTGCTGGCG	ATCGGGTCCG	CGCTCGGTTT	GGAGGGGACC	GTGACCAAGG	GGATCGTCAG	1200
CGTCTCAAC	CGTCCAGTGT	CGAGGACCGG	CGAGGCTGGC	AACGAGAACA	CGGTGCTGGA	1260
CGGCATTGAG	ACCGAGGCGG	CGATCAACCC	CGGTAACTCC	GGGGGCGGCG	TGGTGACAT	1320
GAACGCTCAA	CTCGTGGGAG	TCAACTCGGC	CATTGCTAGG	CTGGGCGGCG	ACTCAGCCGA	1380
TGCGCAGAGC	GCTCCGATCG	GTCTCGGTTT	TGCGATTCCA	GTGACCCAGG	CCAGCCGCT	1440
CGCCGACGCG	TTGATCAGCA	CGGCGAAGGC	GTGACATGCC	TCCCTGGGTC	TGCAGGTGAC	1500
CAATGACAAA	GACACCCCGG	GCCTCAAGAT	CTTCGAAGTA	GTGGCCGCTG	GTCTGCGGCG	1560
GAACGCTGGA	GTGCGGAGG	GCTCTGTTGT	CACCAAGGTC	GACGACCTCC	CGATCAACAG	1620
CGCGGACCGG	TGGTTGCGCG	CGGTGGGCTC	CAAGCGGCGG	GGCGCCAGCG	TGCGGCTAAC	1680
CTTTCAGGAT	CGCTCGGGCG	GTAGCGGCGC	AGTGCAGGTC	ACCTTCGGCA	AGGCGGAGCA	1740
GTGATGAAGG	TGCGCGGCGA	GTGTTCAAGG	C			1771

(2) INFORMATION FOR SEQ ID NO:14:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

CTCCACCCGG GTGGCGGGCG CTCTAGAACT AGTGGATCCU CCGGGCTGCA GGAATTCGGC      60
ACGAGGATCC GACGTCCGAG GTTGTGGAAC CCGCCGDCGC GGAAGTATCG GTCCATGDDT      120
AGCCCGGGCA CCGCGAGCGC CGCAATGGCG CGASTGAGGA GGC GGCGCAAT TTGGCGGGGC      180
CCGGCGACGG CGAGCGCGGG AATGGCGGCA GTGAGGAGGU GGGCAGTCAT GCGCAGGGTG      240
ATCCAATCAA CCTGCATTCC GCGTGGGGGC CCATTTCGCA ATCGAGGTAG TGAGCGGAAA      300
TGAATCATCG AAAACGGGGG GTGACGTCCG CTGTTCTGGT GGTGCTAGGT GCCTGCTTGG      360
CCTTGTGGCT ATCAGGATGT TCTTCGCGCA AACCTGATGC CGAGGACACG GGTGTTCCCG      420
TGAGCCCGAC GSGTCCGAC CCCGCGCTCC TCGCGAGAT CAGGCAGTCG CTTGATCGCA      480
CAAAAGGCTT GACGAGGCG CACGTAGCGG TCGAACAAC CGGGAAGTTC GACAGCTTGC      540
TGGGTATTAC CAGTGGCGAT GTCGACGTCC GCGCCATCC GCTCGCGGCA AAGGGCGTAT      600
GCACCTACAA CGACGAGCAG GTGTCTCCGT TTGGGTACA AGGCGACAC ACCTCGGTGA      660
AACTGTTGCA CGACTGGAGC AATCTGGGCT CGATTCTGA ACTGTCACT TCACGCGTGC      720
TCGATCCTGC CGCTGGGGTG ACGCAGCTGC TGTCCGCTGT CACGAACCTC CAAGCGCAG      780
GTACCGAAGT GATAGACGGA ATTTGACCA CCAAAATCAC CGGAGCCATC CCCGCGAGCT      840
CTGTCAAGAT GCTTGATCCT GCGGCCAAGA GTGCAAGGCC GCGGAGGCTG TGCATTGCCG      900
AGGACGGCTC GCACCACTTC GTCCGAGCGA GCATCGACTT CGGATCCCGG TGATTTCAGC      960
TCACCGAGTC GAAATGGGAC GAACCGGTCA ACGTCGACTA GGCGBAAGTT GCGTCGACGC      1020
GTGATTCGAA ACGGCCCTGT GAACGGTCTC AACGCGAC      1058

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(2) INFORMATION FOR SEQ ID NO:15:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(#1) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA CGAGAGGTGA TGGACATCAT CGGACCCAGC CCCACATCCT GGGAACAGGC	60
GGCGCGCGAG GCGGTCCAGC GGGCGCGGGA TAGCGTCGAT GACATCCGCG TCCTCGGGT	120
CATTGAGCAG GACATGGGCG TGGACAGCGC CGGCAGATC ACCTACCGCA TCAAGCTCGA	180
AATGTCTTTC AAGATGAGGC CGGCGCAGCC GCGTAGCAG GGGCGCGGGA GCAAGACCGA	240
AAATCGCAGC GTTTCGGGT GATTCTGTGC ATTTTGTGTC TGCTCGCGCA GGCCTACGAG	300
GGCGCGCGCA GGTCCGCGTC CTGCGGTATC CAGCGGTGCA TCGCGATTCC GCGCGCGCAG	360
CGCGATTAA TGCTTCGCGT CAGCCGAAAC TGGGCGATCC GCGCGCGAGC TGATCGATGA	420
CGGTGCGCGC CCGCTGATG CCGGATTGC CCGAGGAAAC GTCTTCCAG GCGGTAGGA	480
AGCGTCGTA GCGCGCGGTC CTGACCGGCT CTGCGTCCG CCTCAGTGG GCGAGCGAGC	540
GG	542

(2) INFORMATION FOR SEQ ID NO:16:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 913 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(#1) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGTGCGGCG CGGCGCTCCG TTGCCCCCAT TGCGCCCGTC GCGGATCAGC TGCGCATGCG	60
CACCATCAGC GCGTTTCCCG CCGGACCGCG CGGTGCGGCG GGGGCGCGCG ATGCGACCGC	120
TTGACCGTGG CCGCGCGGCG CGCCATTGCG ATACAGCAGC CCGCGCGGCG CACCGTTACC	180
GCGGTGCGCA CCGTGGCGCG CGTGGCGGTT TCGGCGCGCG GAGGCGGAAT GAGCCGCGCG	240
CAAGCGCGCG GCGGCGCGCG TTGCGCGGTT TTGCGCGCGC CCGCGCGCGC CCGCGATTG	300
CGGACAGCGC AGGACCGGTT GCGCGCGCGC CGCGCGCGGT TAAGCGCGGT CCGCGCGCGC	360
GCGCGCGGAG CCGCATTTAC CGCGGTTGCG GTTGGGTGCG CCGCGGTTAC CCGCGCGCGC	420

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ATTTCGCGCC AATATTCGCG GGGACCGGCU AGACCGGCGG GGGCCACCAT TGCCGCGCGG 480
CACCGAAACA ACAGCCCAAC GTTGGCGGCG GCGCGGCGGT TTGCGGCCAT CACCGGCCAT 540
TCACCGCCAG CACCGCGGTT AATGTTTATG AACCGGTAC CGCCAGCGCG GCGCCATATTG 600
CCGCGCGCGG GAGNGCGTCC CCGCGGCGG CCGCAAGGCG CAAAAGCGCG GGGTTGCCAC 660
CGGCGCGCGG GGACCCACCG GTCCCGCGCA TCGCGCGGTT GCGCGCGGTG CCGCGCGCAT 720
TGGTCTGCTT GAAGCCGTTA GCGCGGTTT CCGCGGTTCC GCGCGGTGCG CCGTGGCGCG 780
CGGCGCGCGG GTTGGCGTAC AGCCACCGCC CGGTGGCGCG GTTGGCGGCA TTGCGGCCAT 840
TGCGCGCGTT GCGCGCATTS CCGCGGTTCC CCGCGCGCAC GCGCGTTGG CCGCGCGCGC 900
CGCGCGCGCG CGC 913

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

GACTACGTTG GTGTACAAA ATCTGCGCG CCGGACCGTT AAGGCTGGA CAATTTCTGA 60
TAGCTACCCC GACACAGGAG GTTACGGGAT GAGGATTCG CGCGCGCGCT CACTCAAGTG 120
GTGATCGTTG CTGAGCTGTC TGCTGCGGT CCGGCTGCGC CTGGCCACGG CCGCGCGCCA 180
GGCGCGCGCG CCGGCTTGT CCGAGGACCG GTTGGCGGAC TTCCCGGCGC TGCCCTCTGA 240
CCGCTGCGCG ATGGTGGCGC AAGTGGCGCC ACAGGTGCTC AACATCAACA CCAACTGGG 300
CTACACACAC CCGGTGGCGC CCGGACCGCG CATCGTCATC GATCCACACG GTGTCGTGCT 360
GACCAACACAC CAGGTGATCG CCGCGCGCAC CGACTCAAT GCGTTCAGCG TCGGCTCCGG 420
CCAAACCTAC GCGGTGATG TGCTCGGGTA TGACCGCACG CAGGATGTG CCGTCTGCA 480
GCTGGCGGCT GCGGCTGCGC TGCGGTGCGC GCGATCGGT GCGGCTGCGC CCGTGGTGA 540
GCGGCTGCTC GCGATGCGCA ACAGCGGTG GCGGCGCGCA ACCCGCGTG CCGTGGCTG 600
CAGGCTGCTC GCGCTGCGCG AAGCGGTGA GCGTGGGAT TCGGTGACCG GTGCGGAGA 660

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GACATTTGAAC GGGTTGATCC AGTTGATGCG CGCAATCCAG CCCGGTGATT CCGGCGGGCC 720
CGTCGTCAAC GGCUTAGGAC AGTGGTCCG TATGACACCG GCCGGGTCCG ATAACCTCCA 780
GCTGTCCACG GGTGGGCAGG GATTGCCAT TCCGATCGGG CAGGCGATGG CGATCGCGGG 840
CCAAATCCGA TCGGGTGGGG GGTACCCAC CGTTCATATC GGGGCTACCG CCTTCCTCGG 900
CTTGGGTGTT GTGACAACA ACGGCAACGG CGGACGAGTC CAAAGCGTGG TCGGAAGCGC 960
TCCGGCGGCA AGTCTCGGCA TCTCCACCGG CGACGTGATC ACCGCGGTGG AGGCGGCTCC 1020
GATCAACTCG GCCACCGGCA TGGCGGACGC GCTTAACGGG CATCATCCCG GTGACGTCA 1080
CTCGGTGAAC TGGCAACCA AGTGGGGCGG CAGCGGTACA GGGAACTGA CATTGGCTGA 1140
GGGACCCCCG GCGTGATTTG TGGCGGATAC CAGTCCCGCG CGGCGCAATT GGATTGGGCG 1200
CAGCGGTGAT TGGCGGTGA GCGCGCGAGT TCGGTCTCCG GTGCGGTGG CATTGTGGA 1260
GCATGAACG AGCGAGACA CAGCGTTGAG CAGGCTCCCG TGCAGGGCAG TTACGTGAA 1320
GGCGGTGTGG TCGAGCATTC GGATGCCAAG GACTTCGGCA GCGCGCGCGC CCTGCGCGCC 1380
GATCGGACCT GGTTTAAGCA CGCGGTCTTC TACGAGGTGC TGGTCCGGGC GTTCTTCGAC 1440
GCCAGCGCGG ACGGTTCCGN CGATCTGCGT GGAATCATCG ATCGCCGCGA CTACCTGCAG 1500
TGGCTTGGCA TCGACTGCA  CTGTTGCCGC CGTTCCTACG ACTCAGCGCT GCGCGACGGC 1560
GGTACGACA TTCGCGACT CTACAAGTG CTGCCCCAAT TCGGCACCGT CGACGATTC 1620
GTGCGGCTGG TCGACACCGC TCACCGGCGA GGTATCCGCA TCATCACCGA CCGGTGATG 1680
AATCACACCT CGGAGTCGA CCGGTGTTT CAGGAGTCCG GCGCGGAGCC AGACGAGCCG 1740
TACGGTGAAT ATTACGTGT GAGCGACAC AGCGAGCGCT ACACGAGCG CCGGATCATC 1800
TTCTGACACA CGAAGAGTC GAACTGGTCA TTGATCCGT TCGGCGACA GTTCTACTG 1860
GCACCGATTC TT 1920

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCSCCGAA	ACCTGATGCC	GAGGAACAGG	GTGTTCCCGT	GAGCCCGAGC	GCTCCGACC	60
CCGCGCTCCT	CGCCGAGATC	AGGCACTCCG	TTGATGCGAC	AAAAGGCTTG	ACCAGCGTGC	120
ACGTAGCGGT	CGGAACCAAC	GGGAAAGTCG	ACAGCTTGCT	GGTATTAC	AGTGCCGATG	180
TGGACGTCCG	GGCCAAATCC	CTCGGGGCAA	AGGGCGTATG	CACCTACAAC	GACGAGCAGG	240
GTGTCCCGTT	TCGGGTACAA	GGCGACAACA	TCTCGGTGAA	ACTGTTGAC	GACTGGAGCA	300
ATCTCGGCTC	GATTTCGTAA	CTGTCAACTT	CACCGGTGCT	CGATCCTGCC	GCTGGGGTGA	360
CGCAGCTGCT	GTCCGCTGTC	ACGAACCTCC	AAGCGCAAGG	TACCGAAGTG	ATAGACGGAA	420
TTTCGACCAC	CAAAATCACC	GGGACCATCC	CCGCGASCTC	TGTCAAGATG	CTTGATCCTG	480
GCCCCAAGAG	TGCAGGCCCC	GGGACCGTGT	GGATTGCCCA	GGACGGCTCG	CACCACCTCG	540
TCCGAGCGAG	CATCGACCTC	GGATCCGGGT	CGATTCAAGT	CACGCACTCG	AAATGGAAAG	600
AACCCGTCAA	CGTCGACTAG	GCCGAAGTTG	CGTCGACCGG	TTGCTCGAAA	CGCCCTTGTT	660
AACGGTGTCA	ACGGCCACCCG	AAACTGACC	CCCTGACGGC	ATCTGAAAAT	TGACCCCTTA	720
GACCGGGCGG	TTGGTGGTTA	TTCTTCGGTG	GTTCGGGCTG	GTGGGACCGG	GCCGAGCTCG	780
CGGTCTTTGA	GCCGCTAGCT	GTGCGCTTTC	AGGGCGACGA	CTTCAGCATG	GTGGACGAGG	840
CGGTGATCA	TGGCGGCGAC	AACGACCTCG	TGCGCGCGGA	AAACCTCGCC	CCACCGGCGG	900
AAGSCCTTAT	TGGACGTGAC	GATCAAGCTG	GCCCGCTCAT	ACCGGGAGGA	CACCAGCTCG	960
AAGAAGAGGT	TGGCGGCGTC	GGGCTCAAAC	GGAAATGTAAC	CGACTTCGTC	AACCACCAGG	1020
AGCGGATAGC	GGCCAAACCG	GGTGAAGTTC	GGTACATCC	GGCGGCGGTG	GTGAGCCTCG	1080
GGGAACCTG	CTACCCATTC	GGCGGGGGTG	GGGAACAGCA	CCCGATGACC	GGGCTGACAC	1140
GCGCGTATCG	CCAGGCTGAC	CGCAAGATGA	GTCTTCCCGG	TGCCAGGCGG	GGCCCAAAAA	1200
CACGACGTTA	TGCGGGGCGG	TGATGAAATC	CAGGGTGCCC	AGATGTGCGA	TGGTGTGCGG	1260
TTTGAGGCGA	CGAGCATGCT	CAGAGTCGAA	CTCTTCCAAC	GACTTCGAA	CCGGGAAGCG	1320
GGCGGCGGCG	ATGCGGCGCT	CACCACCATG	GGACTCCCGG	GCTGACACTT	CCGCTGCGAG	1380
GCAGGCGGCG	AGGTATTCTT	CGTGCGCTCA	GTCTCGGCGG	CGGGCGCGAT	CGGCCAGCGG	1440
GGACACTGAC	TCAAGCAGGG	TGGGAGCTTT	CAATGCTCTT	GT		1482

(2) INFORMATION FOR SEQ ID NO:19:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 876 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAAATTCGGCA	CGAGCCGGCG	ATAGCTTCTG	GGCCGCGGCC	GACCAAGATGG	CTCGAGGGT	60
CGTGCCTCGG	GCCACCGGCG	GGCSCACCAC	CGTACCGGT	GAGGGGCTGC	AACACGCCGA	120
CGGTCACTCG	TTGCTGCTCG	ACGCCACCAA	CCCGGCGGTG	GTTGCCTACG	ACCCGGCCTT	180
CGCCTACGAA	ATCGGCTACA	TCGNGGAAAG	CGGACTGGCC	AGCATGTGCG	GGGAGAACCC	240
GGAGAACATC	TTCTTCTACA	TCACCGTCTA	CAACGAGCTG	TACGTGCAGC	CGCCGAGGCC	300
GGAGAACTTC	GATCCCGAGG	GGTGCCTGGG	GGGTATCTAC	CGTATCACCG	CGGCCACCGA	360
GCAACGCACC	AACAAGGAGC	AGATCCTGGC	CTCCGGGGTA	GCGATGCCCG	CGGCGCTGCG	420
GGCAGCACAG	ATGCTGGCGG	CCGAGTGGAA	TGTGCGCGCC	GACGTGTGGT	CGGTGACCCAG	480
TTGGGGCGAG	CTAAACCGCG	ACGGGGTGGT	CATCGAGACC	GAGAAGCTCC	GCCACCCCGA	540
TGGGCGGGCG	GGCGTGGCCCT	ACGTGACGAG	AGCGCTGGAG	AATGCTCGGG	GCCCGGTGAT	600
CGCGGTGTGG	GACTGGATGC	GCGCGGTCCC	CGAGCAGATC	CGACCGTGGG	TGCGGGGCAC	660
ATACCTCAGG	TTGGGCACCG	ACGGGTTGCG	TTTTTCCGAC	ACTCGGCCCC	CGCGTGGTGG	720
TTACTTCAGC	ACCGAGCGCG	AATCCAGGT	TGGTCEGGT	TTTGGGAGGG	GTTGGCCGSG	780
TGACGGGGTG	AATATCGACC	CATTGGGTGC	CGGTGGTGGG	CGCCCGCCCC	AGTTACCCGG	840
ATTGACGAGG	GGTGGGGGGT	TGGGCCCGAN	TAAGTT			876

(2) INFORMATION FOR SEQ ID NO:20:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1021 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCCCCCGCG	GCTGCAGGAA	TTGGGCACGA	GAGACAAAT	TCCACCGGTT	AATGCAGGAA	60
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CAGATTCATA	ACGAATTCAC	AGCGGCACAA	CAATATGTGG	CGATCGCGGT	TTATTTGAGC	120
AGCGAAGACC	TGCGCGAGTT	GGCGAAGCAT	TTTTACAGGC	AAGCGGTGGA	GGAACGAAAC	180
CATGCAATGA	TGCTCGTGCA	ACACCTGCTC	GACCGCGAGC	TTCGTGTGGA	AATTCGCGGC	240
GTAGACACGG	TGCGAAACCA	GTTCGACAGA	CCCCGCGAGG	CACTGGCGCT	GGCGCTCGAT	300
CAGGAACCCA	CAGTCACCGA	CCAGGTGGGT	CAGCTGACAG	CGGTGGCCCG	CGACGAGGGC	360
GATTTGCTCG	GCGAGCAGTT	CATGCGGTGG	TTCTTGCGAG	AACAGATCGA	AGAGGTGGCC	420
TTGATGGCAA	CCCTGGTGCG	GTTTGCCGAT	CGGCGCGGGG	CCAGCTGTGT	CGACCTAGAG	480
AACTTCGTCC	CAGGTGAAGT	GGATGTGGCG	CGGCGCGCAT	CAGGCGCCCC	GCACGCTGCC	540
GGGGGGCCCC	TCTAGATCCC	TGGGGGGGAT	CAGCGAGTGG	TCCGTTTGGC	CCGCGCGTCT	600
TCCAGCCAGG	CCTTGCTGCG	GCGGGGGTGG	TCAGTACCAA	TCCAGGCCAC	CCCGACCTCC	660
CGGNAAGAST	CGATGTCTTC	GTACTCATCG	ACGTTCCAGG	AGTACACCGC	CCGCGCTTGA	720
GCTGCCGAGC	GGTCAACGAG	TTGCGGATAT	TCCTTTTACG	CAGGCAGTGA	GGGTCCCACG	780
GCGGTTGGCC	CGACCGCGGT	GCGCGCACTG	CTGGTCAGGT	ATCGGGGGGT	CTTGCCGAGC	840
AACAACGTCC	GCAGGAGGGG	TGGAGCCCGC	CGGATCCGCA	GACCGGGGGG	GCGAAAACGA	900
CATCAACACC	GCACGGGATC	GATCTCCGGA	GGGGGCTGCG	GGAATACCGA	ACCGGTGTAG	960
GAGCGCCAGC	AGTTGTTTTT	CCACCAGCGA	AGCGTTTTTC	GGTCATCGGG	GCNNTTAAG	1020
T						1021

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTCCCGAGC	AACGGAAGAA	CACAACCATG	AAGATGTTGA	AATCGATCGC	CGCAGGTCTG	60
ACCGCGCGCG	CTGCAATCGG	CGCGGCTGCG	GCGGCTGTGA	CTTCGATCAT	GGCTGGCGGN	120
CGGTCGTAT	ACCAGATGCA	GCGGCTGCTC	TTGCGCGCGC	CACTGCGGTT	GGACCGGNA	180

TCGGCCCCCTG AAGTCCCCGAC CCGCCCCCAG TGGACCAAGC TGCTCAACAG NCTCGNCGAT 240
 CCGAACGTGT CATTGNGAA CAAGGAGACT CTGTCGAGG GNGGNATCGG NGGNANGAG 300
 GGNNGNATC GNGGACACA A 321

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATCGGT TCCGTTGGC GACGGCTTTF GCGNCGGGT GGTAAACXG CTCGGCCAGC 60
 CGATCGACCG GCGCGGAGAC GTCGACTCG ATACTCGCG CGCGCTGGAG CTCGAGGCGC 120
 CUTCGGTGGT GNACCCGCA GCGGTGAAG AGCGTTGNA GACCGGGATC AAGGCCATTC 180
 ACGCGATGAC CCGATCGGC CCGGGGACGC GCCAGCTGAT CATCGGGGAC CGCAAGACCG 240
 GCAAAAACCG CCGTCTGTGT CCGACACCAT CCTCAACCA GCGGGAAGAA CTGGGAGTCC 300
 GGTGGATCCC AAGAAGCAG TCGGCTTGTG TATACCTTG CCATCGGGCA AGAAGGGGAA 360
 CTTACCATCG CCG 373

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACCGCGT CATGGGATTC CTGGGCGGGG CCGGTCCGCT GCGGTGGTG GATCAGCAAC 60
 TGGTAAACCG GGTGCGGCA GCGTGGTGG TTGCTCAGGC AGCGCTGTG CCGGTGGTGT 120
 TCTTACGGC CTGGTACGG TTGCGCATT TAGCCGAGAT CAGCGGGGC GAATCGGTGC 180
 TGATCCATCC CGGTACGGC GGTGTGGCA TCGCGCTGT GCAGCTGGCT CGCCAGTGGC 240

GCGTCGAGGT TTTCGTCACC GCCAGCCGTC GNAAGTGGGA CACGCTGCCC GCCATNGNGT 300
 TTGACGACGA NCCATATCGG NGATTCCGNC ACATNCGAAG TTCGAGGGA GA 352

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCCGCC TTCATTCCGT TCGACCAGCG GCTGGGATA ATCGACGAG TGATCAAGCC 60
 GCGGTTCCGG GCGCTCATGG CTCACAGGCA GTAATCAGCA AGTTCTCTGG TATATGGCAC 120
 CTAGCGTCCA GTTCTTGGC AGATCGCTT CGTACCCTCA TCGCATGTAC CGTTTCGGT 180
 GCGCACGCT CATGCTGGCG GCGTGCATCC TCGCCAGGG TGTGGCGGGT CTCGGGGTGG 240
 GCGCGCAGTC CGCAGGCCAG ACCGCGCCGG TGCCGAGTA CTACTGGTGC CCGGGGCAGC 300
 CTTTCGACCC CGCATGGGGG CCGACTGGG ATCCCTACAC CTGCCATGAC GACTTCACCC 360
 GCGACAGGCA CGGCCCGAC CACAGCCGCG ACTACCCCGG ACCCATGCTC GAAGGTCCCG 420
 TGCTTGACCA TCCCGGTGCT GCGCCGCCCC CCGGGCTGC CGGTGGCGGC GCATAGCGGT 480
 CGTTGAGCGG GCGGCATCAG CGATACGCG TATAAAGCCG GCGGTGCCCC CGGCAAGCTA 540
 CGACCCCCCG CGGGGAGAT TTACGCTCCC GTGCCATGG ATCGCGCGGT CGATGACAG 600
 AAAATAGGCG AGGTTTTTGG CAACCGCTG GAGGACGCTT GAAGGGAGCC TGTATGAAC 660
 GCGACAGCG CCTCCACCAT CGACATGAC AAGGTTGTTA CCGGCACACC CGTTGCCCCG 720
 ATCGTG 726

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

CGCGAAGGAGG ACGAAGCTCG GGGCCACCAC CGGCTATGCG TTGATGCAGG CGACCGGAGT      60
GGTGGGCGGAC CATATCCAAG CATGCTGGGT GGGCACTGAG CGACCTTTTG ACCAGCCGGG      120
CTGCCCCGATG GGGGGCCGGT GAAGTCATTG CCGCGGGGCT TGTGCACCTG ATGAACCCGA      180
ATAGGGAACA ATAGGGGGGT GATTTCGCAG TTCAAATGTCG GGTATGGCTG GAAATCCAAT      240
GGCGGGGCGAT GTCGCGGCGC GACCAGGCTC GCGCAGGCGG GCCAGCCCGA ATCTGGAGGG      300
AGCACTCAAT GCGGGCGATG AAGCCCCGGA CCGGCGACCG TCCTTTGGAA GCACTAAGG      360
AGGGGCGCGG CATTGTGATG CGAGTACCAC TTGAGGGTGG CGGTGCGCTG CTCGTGAGC      420
TGACACCCGA CGAAGCCGCG CCACTGGGTG ACGAACTCAA AGGCGTACT AGCTAAGACC      480
AGCCCAACCG CGAATGGTGG GCGTTACGCG CACACCTTCC GGTAGATGTC CAGTGTCTGC      540
TCGGCGATGT ATGCCLAGGA GAAGTCTTGG ATACAGGCGT      580

```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

AACGGAGGCG CCGGGGGTTT TGGCGGGGCG GGGCGGGTGG GCGGCAACCG CCGGGCCGGC      60
GGTACCCCGG GATTGTTCGG TGTGCGCGGG GCGGCTGGGG CCGGAGCCAA CGGCATCGCC      120
GGTGTCAGGG ATACGTGGGC CAGCACACCG GGTGGATCCG      160

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

GACACCGATA CGATGGTGAT GTACGCCAAC GTTGTGGACA CGCTCGAGGC GTTCACGATC      60
CAGCGCACAC CCGACGGCGT GACCATCGGC GATGCGGGCC CGTTGGCGGA GGCGGCTGCC      120
AAGGCGATGG GAATCGACAA GCTGCGGGTA ATTCTATCCG GAATGGACCC CGTCGTGGCT      180
GAACCGCAAC AGTGGGACGA CGGCAACBAC ACCTTGGCGT TGGCGCCGGG TGTCTTTGTC      240
GCCTACGAGC GCAACCTACA GACCAACCCC CG                                272

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(2) INFORMATION FOR SEQ ID NO:28:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

GCAGCCGGTG GTTCTCGGAC TATCTGCCCA CGGTGACGCA GCGCGACGTG CGCGAGCTGA      60
AGCGGATCGA GCACACGGAT CGCTTGCCGC GGTTCATCGG CTACCTGSCC GCTATCACCG      120
CGCAGGAGCT GAACCTGGCC GAACCGGCGC GGCTCATCGG GGTCCAGCGG GGGACGATCC      180
GTTCCGATCT GGCCTGGTTC GAGACGGTCT ATCTGGTACA TGGCTGCCC GCCTGGTCGC      240
GGAATCTGAC CGCGAAGATC AAGAAGCGGT CAAAGATCCA CGTCGTGAC AGTGGCTTCC      300
CGCCCTGGTT GCGCGGC                                317

```

(2) INFORMATION FOR SEQ ID NO:29:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

GATCGTGGAG CTGTCCATGA ACAGCTTGC CGGACGCGCG GCGGCCAGCA CGTCGGTGTG      60

```

GCAGCGCCCG	ACACCTCGC	CGGTGGGAG	CATGGTATG	ACCACGTCG	CCTCGGCCAC	120
CGCTTCGGG	GCCTACGAA	ACACCGGAC	ACCGTGGCG	CGGGCGCCG	ACGGCGCGT	180
GG						182

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCGCGAAG	TTGGTGAGC	AGGTGCTCA	CGCGAAGTC	TGGCGGCTG	CGAAGCGGT	60
CGCGGTTTAC	GAGGCGAAGA	CACGCTGTC	CGAGCTGCTG	CGGCTCGTCT	ACGGCGGGCA	120
GAGGTTGAGA	TTGCCCCCG	CGGCGAGCC	GTAGCAAGC	TTGTGCCCT	GCATCCTCAT	180
GAGACTCGGC	GTTAGGCAT	TGACCATGG	GTGTACCGG	TGCGGACGA	TTTGGAGCT	240
CCGTTGTCA	ACGAGCTGCT	CGACCGCTT	CACCGTGA	GGCTACCTC	ATCGACACCC	300
ACGTTTGG						308

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCGACGACGA	GCACTCAG	TGGATGATG	TGGCAGCGG	CATTGAGGAC	GGAGAGAATC	60
CGGCGGAGC	TGCGCGCGG	CAAGTCTCA	TAGTACCGG	CGGTAGAGG	CTCCCCGAT	120
GGACCGGAC	TATTCTGCTG	TGCGCTGGC	CGGTAGAGC	GGTTAAGA	ATGTGAGGG	180
ACACGATGAG	CAATCACAC	TACCGAGTG	TGAGATCGT	CGGACCTCG	CCCCACGGG	240
TGGACGGGG	ATCCAGGG	GCTCTG				267

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

CTCGTGCCTG  AAGAATCTGA  GGGGACACGA  TGGCAATCA  CACCTACCGA  GTGATCGACA      60
TCGTCCGGAC  CTCCTCCGAC  GCGTCCAGG  CCGCAATCCA  GGGCGGTCTG  GGCUGAGCTG     120
CGCAGACCAT  GCGCGCGCTG  GACTGGTTTG  AAGTACATC  AATTCGAGGC  CACCTGGTCTG     180
ACGGAGCGGT  CCGGCACTTC  CAGGTGACTA  TGAAGTCCG  CTTCGGCTCG  AGGATTCCTG     240
AACCTTCAG  CCGCGCCGAT  AACTSAGGTG  CATCATTAAG  CGACTTTTCC  AGAACATCCT      300
GACGCGCTCG  AAACCGCGTT  CAGCCGACGG  TGGCTCCGCG  GAGGCGGTGG  CTCCAAAATC      360
CCTGCGACAA  TTCCTCGGCG  GCGCTACAA  GGAAGTGGT  GCTGAATTGG  TCGGGTATCT      420
GGTCGACCTG  TGTGGGCTGC  AGCCGACGGA  AGCGGTGCTG  GAGGTCCGCT  GCGGCTCGGG      480
GUGGATGCG  TTGCGGCTCA  CCGCTATCT  GAACAGCGAG  GGACGCTACG  CCGGCTTCGA      540
TATCTCGCAG  AAAGCCTATG  GGTGTTGCA  GGAGCAGATC  ACCTCGGCGC  ACCCCAACTT      600
CCAGTTCGAG  GTCTCCGACA  TCTACAATC  GCTGTACAAC  CCGAAAGGGA  AATAACAGTC      660
ACTAGACTTT  CGCTTTCAT  ATCCGATGC  GTCTTTCAT  GTGGTGTTC  TTACCTCGGT      720
GTTACCCAC  ATGTTTCCG  CCGACCTGA  GCATATCTG  GACGAGATCT  CCGGCTGCT      780
GAAGCCGCG  GACCATGCC  TGTGACGTA  CTCTTGTCT  AATGACGAT  CTTAGCCCA      840
CATCGCGGAA  GGAAGAGTG  CGCACAAT  CCAGCATGAG  GGACCGGCTT  ATCGGACAT      900
CCCAAGAG  CGGCCGAG  AGCAATCG  CTTGCCGAG  ACCTTCCTCA  GCGATGTCTA     960
TGGCAAGTTC  GCGCTCGCG  TGCAGAAC  ATTCCACTAC  GCTCATGA  GTGGCCGGA     1020
ACCAGCCTA  AGCTTCCAG  ACATCTCAT  CCGAGCCAAA  ACCGCGAGCT  AGGTCTGGCAT     1080
CUGGGAAGCA  TCGGACACC  GTGGGCGGA  GCGCGCTTC  CCGCAGGCG  ATTAGGCGG     1140
CAGATTAGCC  CCGGCGGCT  CCGGCTCG  AGTACGCGC  CCGAATGG  CTCACCGGCT     1200
GGAACCAAG  CTTCGCGCG  TGGCGCGCG  CTTCCCGAT  CAGGTGCTAG  ATCCCGACAA     1260

```


AGCCTGCGTG	ATCGGTGATC	ACCAACGGTG	ACAGCAGCCG	GTTGTGCACC	AGCGCGAAGC	1320
CCACCCCGGT	CTCGGGGTCT	GTCCAGCCGA	TCGAGCCGCC	CAAGCCACAC	TGACCAAAAC	1380
CCGCGATCAC	GTTGCCGATC	GGCATACCGT	GATAGCCAAAG	ATGAAAATTT	AAGGGCACCA	1440
ATAGATTTCG	ATCGGCGAGA	ACTTCCCGTC	GGTTCGGGGT	CAGGCCCGTG	ACCAGCTCCC	1500
GCGACAAGAA	CCGTATGCCG	TCGATCTCGC	CTCGTSCCG			1539

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCAGGGTG	GCGTGCATGA	GCGTCACCGC	GGGSCAGGCC	GAGCTGACCG	CCGCCAGGT	60
CCGGGTTGCT	GCGGGGGGCT	ACGAGACGGC	GTATGGGCTG	ACGGTGGCCC	CGCCGTTGAT	120
CGCCGAGAAC	CGTCTGAAC	TGATGATTCT	GATAGCGACC	AACCTCTTGG	GGCAAAACAC	180
CCCGGCGATC	GCGGTCAACG	AGGCCGAATA	CGGCGAGATG	TGGGCCCAAG	ACGCGGCCGC	240
GATGTTTTGC	TACGCCGGCG	CGACGGCGAC	GGCGAGGGCG	ACGTTGCTGC	CGTTGAGGA	300
GGCGCCGGAG	ATGACCGCG	CGGGTGGGCT	CTTCGAGCAG	GCCGCCGCGG	TGGAGGAGGC	360
CTCCGACACC	GCGCGCGCGA	ACCACTTGAT	GAACAATGTG	CCCCAGGCGC	TGAAACAGTT	420
GGCCAGCCCC	ACGCGGGCCA	CCACCCCTTC	TTCCAAAGCTG	GGTGGGCTGT	GGAAGACGGT	480
CTCGCCGCAAT	CGGTGCGCGA	TCAGCAACAT	GGTGTGATG	GCCAACAACC	ACATGTCGAT	540
GACCAACTCG	GGTGTGTGGA	TGACCAACAC	CTTGAGCTCG	ATGTTGAAGG	GCTTTGCTCC	600
GGCGGCGGCC	CCCCAGGCGG	TGCAAAACCGC	GGGCGAAAAC	GGGGTCCGGG	CGATGAGCTC	660
GCTGGGCGAG	TGCTGGGCTT	CTTCGGGTCT	GGGCGGTGGG	GTGGCGGCGA	ACTTGGGTCC	720
GGCGGCTTCG	GTACGGTATG	GTCACCGGGA	TGCGGGAATA	TATGCANAGT	CTGCTCGGCG	780
GAACGGTGGT	CCGGCGTAAAG	GTTTACCCCC	GTTTTCTGGA	TGCGGTGAAC	TTCGTCAACG	840
GAAACAGTTA	C					851

(2) INFORMATION FOR SEQ ID NO:34:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCGATCGG	GCGGAAATTT	GGACGAGATT	CGCCTCCGGC	GATAACCCAA	TCAATCGAAC	60
CTAGATTTAT	TCCCTCCAGG	GGCCGAGTA	ATGCTCGCA	GGAGAGGAAC	CTTACTGCTG	120
CGGGCACCTG	TGGTAGGTCC	TCGATACGGC	GGAGGCGTC	GACATTTTCC	ACCGACACCC	180
CCATCCAAAC	GTTCCAGGGC	CACTCCAGCT	TGTGAGCGAG	GCGACGCAGT	CCGAGGCTGC	240
GCTTGSTCAA	GATC					254

(2) INFORMATION FOR SEQ ID NO:35:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCCTGACC	GAGCGGGCGG	CCGCCAAGGC	GAAGTCGCTG	TGGGACCAGG	AGGGACGGGA	60
CGATCTGGCG	CTGCGGATCG	CGTTTCAGCC	GGGGGGGTGC	GCTGGATTGC	GCTATAACCT	120
TTTCTTCGAC	GACCGGACGC	TGATGCTGA	CCAAACCGCG	GAATTGCGTG	GTGTCAGGTT	180
GATCGTGGAC	CGGATGAGCG	CCCCGTATGT	GGAAGGCGCG	TGATCGATT	TGTTCCACAC	240
TATTGAGGAG	CAAGGTTTAC	CATGGACAAT	CCCAACGGCA	CCGGCTCCTG	CGCCTGCGGG	300
GATTGCTTCA	ACTGATAAAA	CGTAGTACG	ACCCCGGGGT	GCGCACACCG	TACGAGCACA	360
CCAAGACCTG	ACCCGCTGG	AAAAGCAACT	GAGCGATGCC	TTGCACCTGA	CCGCGTGCGG	420
GGCGGCGGCG	GGCAGGTGTC	ACCTGCATGG	TGAACAGCAC	CTGGGCTGTA	TATTCCGACC	480
AGTACAGGAT	TTTGTGATC	GAGGTCACTT	CGACCTGGGA	GAACTGCTTG	CGGAACGCGT	540

```

CGCTGCTCAG CTTGCCCAAG GCGTGATCGG AGGCGTTGTC GCGCAGCCCG TCGTGGATAC      600
CGCACAGCGC ATTGCGAAGC ATGCTGTGCA CAGCGCGGTT CTCCAGCGCG TTGAGGTATC      660
CCTGAATCGC GCTTTTGGCC GGTCCCTCCG AGAATGTGCC TGGCGTGTTC GCTCCGTTGG      720
TGGGACCCCG GTATATGATC GCGGCGGTCA TAGCCGACAC CAGCGCGAGG GCTACCACAA      780
TGGGATCAG CAGCCGTTT TCGGTGCGT TCGGTAGGA CAGCTGCGGC GGCACGCGCG      840
GATATGCGGC GGGCGGTCAC GCGCGCTCGT CTGCGCGTCC CGGGCGGAGG GCGGTTGCG      900
CGGCGCGGAG GTGCTGGGG TAGTCCAGG CTTGGCGTTC GTGGGATGAG GCGTGGGGT      960
AGGGCGCGGG TCGTTGGTG CCGACACCGG GGTTCGCGGA GTGGGGACCG GGCATTGTGG     1020
TTCTCCTAGG GTGCTGGAGC GGACGAGCTG CTAGGGCGAC AACCGGCGCT CGGCTCAGCC     1080
GGCAGCATCG GCAATCAGGT GAGCTCCCTA GCGAGGCTAG CGCAACAGCT GCGCTCGCT      1140
CTCAACCGCA CGGGCGCGGC CGCGGCGCGG ATAATCTTGA AAGACTAGGC AACCTTAGCA     1200
ACGAAGGACG GAGATTTTGT GACGATC                                     1227

```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

GCGGTGTCCG CGGATCCGCG GGGTGGTTGA AGGGCAACGG CGGGGCGGCG GGGGCGGGG      60
GGACCGGCGC TAACGGTGGT GCGGCGGCGA AGGCTCGTT GTTCGGGCGC GCGGGGTCCG     120
GCGGCGCGCG CACCAATCGT CGGCTCGCGG GTTCGCGCGG ATTTGTCTAC GCGACCGGCG     180
G                                     181

```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

GGGTGTCTCG CCGATCCGGC GGCTGGTTGA ACGGCACCGG CGGTGTCTCGG GCGCGGGGCG      60
GCGACGGCCT CTTCGCGGT GCGGGCGGCG AGGGCGGCGT CGGTGGGCAG GCGGCAATG      120
GCGGCGGCTC CACCGGCGGC AACGGCGGTC TTGGCGGCGC GCGCGGTGGC GGAGGCAACG      180
CCCCGGACGG CGGCTTCGGT GSCAACGGCG STAAGGCTGG CCGGGGCGGN ATTGGCGGCG      240
GCACTCAGAG CCGGACCGCG CTCGGGCGTG ACGGCGGTGA CCGCGGTGAC      290

```

(2) INFORMATION FOR SEQ ID NO:38:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

GATCCAGTGG CATGCGGGT GTCACTGGAA GCAT      34

```

(2) INFORMATION FOR SEQ ID NO:39:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

GATCGCTGCT CGTCCCCCCC TTGCGGCGGA CGCCACCGGT CCCACCGTFA CCGAACAAAC      60
TGGCGTGGTC GCGAGCACCC CGGACACCGC CGACGCGCGA GTCGAACAAT GGCACCGTCC      120
TATCCGACAC ATTGCGGCGG GNCCTACCGG CACCG      155

```

(2) INFORMATION FOR SEQ ID NO:40:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGTCGTTCA CGGGGCGCCG GGGACCGGGC AGCCCGGNGG GCGCGGGGGG TGG 53

(2) INFORMATION FOR SEQ ID NO:41:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCCACCGC GGGTGCAGAC GGTGCCCCCG GCGCCACCCC GACCGGCGGC GGCAACGCGC 60
 GCACCGGCGG CAACGCGCGG AACGCCACCG TGTCTGGNGG GCGCGGCGGG GCGGCGGCGA 120
 AGGCGCGCAA CG 132

(2) INFORMATION FOR SEQ ID NO:42:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCGGCGGC CGGACGGGC GGGGACGGCG GCAAGGCGCG NAACGGGGGC GCGGACGCGA 60
 CCGGCCAAGA ATCTCCGNG TCCNCCATG GCGCGAATGG CGGACGGGC GGCAACGGCG 120
 GCACGGCGCG CA 132

(2) INFORMATION FOR SEQ ID NO:43:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

CGGCACGAGG ATCGGTACCC CCGGCATCG GCAGCTGCCG ATTCGCCCGG TTCCCCCACC      60
CGAGGAAAGC CCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCGGTTCG CGATGCCGCG      120
ATGAACGGCC GGCATCAAAT TAGTGCAGGA ACCTTTCAGT TTAGCGACGA TAATGGCTAT      180
AGCACTAAGG AGGATGATCC GATATGACGC AGTGGCAGAC CGTGACGGTG GATCAGCAAG      240
AGATTTTGA CAGGGCCAAC GAGGTGGAGG CCGCGATGGC GGACCCACCG ACTGATGTCC      300
CCATCACACC GTGCGAACTC ACGGNGGNTA AAAACGCCGC CCAACAGNTG GTNTTGTCCG      360
CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAGA GGGGCAGCCT CTGGCGACCT      420
CGCTGGCGAA CCGGCCCAAG GNGTATGGCG AGCTTCATGA GGAGGCTGCC ACCGCGCTGG      480
ACACCGACCG CGAAGGAACT GTCCAGGCTG AATCGGCCCG GCGCGTCCGA GGGACAGTTC      540
CGGCGGAATC AACCGATACG CCGAGGGTGG CTACGCGCGG TGAACCCAAC TTCATGGATC      600
TCAAAGAGGC GGCAGGAAG CTCGAACGG GCGGCCAAGG CGCATCGCTC GCGCACTGNG      660
GGGATGGGTG GAACACTTNC ACCCTGACGC TGCAAGGCCA CG                                702

```

(2) INFORMATION FOR SEQ ID NO:44:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

GAGCGCCGAG CGCTGTCCGG CGACGTGGCG GTCAAAGCGG CATCGCTCGG TGGCGTCCA      60
GGCGCGCGGG TGCGTCCGC GCGGTGGGA TCCCGATCG GGGGCGCCA ATCGGTCCCG      120
CCCTCTGCCG CTGCTGACAT TCCCGGTTA GCGCAGGAA GGGCGCGCGG CCGCGCGCGG      180

```

CTGGGCGGGG	GTGGCATGGG	AATGCCGATG	GGTGCCGCGC	ATCAGGGACA	AGGGGGGGGG	240
AAGTCCACGG	GTTCCTCAGC	GGAGACGGAG	GCGCTCTACA	CCGAGGATCC	TCGTGCGG	298

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGCACGAGG	ATCGAATGCG	GTGGCGGGGA	GCACAGCGTC	GCACTGCACC	AGTGGAGGAG	60
CCATGACCTA	CTGGCGGGGT	AACCGCGGAT	ACCGCGAAGC	GCAGCCCGCA	GGCTCCTACG	120
GAGGCGTCAC	ACCTTCGTTT	GCCCACGCGG	ATGAGGGTGC	GAGCAAGCTA	CCGATGTACC	180
TGAACATCGC	GGTGGCAGTG	CTGGGTCTGG	CTGCTACTTT	CGCCAGCTTC	GGCCCAATGT	240
TCACCCTCAG	TACCGAATTC	GGGGGGGGTG	ATGGCGCAGT	GTCCGGTGAC	ACTGGGCTTC	300
CGGTGGGGGT	GGCTCTGCTG	GCTGCGCTTC	TGCGCGGGGT	GGTCTGCTTG	CCTAAGGCCA	360
AGAGCCATGT	GACGCTAGTT	GCGGTGCTCG	GGTACTCGGG	CGTATTCTTG	ATGGTCTCGG	420
CGACCTTTAA	CAAGCCCGAG	GCCTATTGGA	CGGGTGGGGC	ATTGTGGGTT	GTGTGGGCTT	480
TCACTGCTTT	CCAGGCGGTT	GCGGCAGTCC	TGGCGCTCTT	GGTGGAGACC	GGCGCTATCA	540
CGCGCGCGGC	GGCGCGGGCC	AAGTTCGACC	CGTATGAGCA	GTACCGGGCG	TACGGGCAAT	600
ACGGCCAGTA	CGGGGTGCAG	CGGGGTGGGT	ACTACGGTCA	GCAGCGTGCT	CAGCAGGGCG	660
CGGACTGCA	GTGGCGGGCC	CGGCAGCAAT	CTCCGCAGCC	TGCGCGATAT	GGGTGCGAAT	720
ACGGCGGCTA	TTGCTCCAGT	CGGCGCAAT	CGGCGAGTGG	ATACACTGCT	CAGCCCCCTG	780
CCGAGCGGGC	GGCGCAGTCC	GGGTGCGAAC	AATGCGACCA	GGGCGCATCC	ACGCCACCTA	840
CGGGCTTTTC	GAGCTTCAGC	CCACCGCCAC	CGGTCACTGC	CGGCGAGGGG	TGCGAGGCTG	900
GTTCGGCTTC	AGTCAACTAT	TCAAACCCCA	GCGGGGGCGA	GCACTGCTCG	TGCGCGGGGG	960
GGGCGCGGGT	CTAACCGGGC	GTCCCGGGGT	CGGCTCGCGC	GTGTGCGCGA	AGAGTGAGCA	1020
GGGTGTCAGC	AGCGCGGGAC	GATCCTGCTG	CGGAATTC			1058

(2) INFORMATION FOR SEQ ID NO:46:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(*1) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

CGGCACGCGA GACCGATGCC GCTACCCCTCG CCGAGGAGGC AGGTAAATTTC GAGCGGATCT      60
CGGCGGACCT GAAAAACCCAG ATCGACCAGG TGGAGTCGAC GGCAGCTTCG TTGCAGGGCC      120
ACTGGCGCGG CCGCGCCGGG ACGGCCGCCC AGGCGCGGCT GTTSCGCTTC CAAGAAGCAG      180
CCATAAGCA GAGGCAGCAA CTCGACGAGA TCTCGACGAA TATTGGTTCG GCGGGCGTCC      240
AATACTCGAG GCGTCAGCAG GAGCAGCAGC AGGCGCTGTC CTCCCAATG GCGTTCTGAC      300
CCGCTAATAC GAAAGAAAC GGAGCAA                                327

```

(2) INFORMATION FOR SEQ ID NO:47:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 170 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(*1) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

CGGTCCCAT GATGGCTTC TCGAACGTGA CCGATTCTGT ACCGCCCTCG TTGAGATCAA      60
CCAACAACGT GTTGGCTTC GCAATGTGC CGNACCGTGG GATTCGGGTG ATCTTGTCT      120
TCTTCATCAG GAAGTCACG CCGGCCACCC TCGCCTCGG TACCTTTGG      170

```

(2) INFORMATION FOR SEQ ID NO:48:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

GATCCGGCGG CACGGGGGGT CCGGGCGGCA GCACGGCTGG CCTGGGCGG AACGGCGGG      60
CGGGGGGTGG CGCGCGAACC GGTGGGTTC TCTTCGGCAA CGGCGGTGCC GCGGGGCACG      120
GGGCGGT                                           127

```

(2) INFORMATION FOR SEQ ID NO:48:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

CGGCGCAAG GGGCGACCG CCGCAACCG GAGCGGCGG GCGGCGGCA ACGGCGGCA      60
CGGCGGCTCC GGCTCAACG G                                           81

```

(2) INFORMATION FOR SEQ ID NO:49:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

GATCAGGGCT GCGCGGCTCC GGCAGAAAG GCGTAACGG AGGAGCTGCC GGATTGTTG      60
GCACGGGCGG GCGCGGGGT GCGGCGGCT CCAACCAAG CCGTAACGG GGGCGGCGG      120
GAAACGGTGG TGCGGTGGG CTGATCTGG                                           149

```

(2) INFORMATION FOR SEQ ID NO:51:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGCACGAGA TCACACCTAC CGAGTGATCG AGATCGTCGG GACCTCGCCC GACGGTGTGG	60
ACGCGGNAAT CCAGGGGGGT CTGGCCCGAG CTGGCGAGAC CATGCGCGCG CTGGACTGGT	120
TGGAAGTACA GTCAATTGGA GGCCACCTGG TCGACGGAGC GGTCCGCGAC TTCCAGGTGA	180
CTATGAAACT CGGCTTCGGC CTGGAGGATT CTTGAACCTT CAAGCGCGGC CGATAACTGA	240
GGTCATCAT TAAGCGACTT TTCCAGAGCA TCTGACCGG CTCGAAACGC GGTTCAGCGG	300
ACGCTGGCTC CGCGAGGCG CTGGCTGCAA AATCCCTGCG ACATTCGTC GGCGG	355

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCACC ATCACCATCA CATGCATCAG GTGGACCCCA ACTTGACACG TCGCAAGGGA	60
CGATTGCGCG CACTGGCTAT CCGGGGATG GCGAGCGCCA GCGTGCTGAC CGTTGCGGTG	120
CGCGCGACCG CCAAGCGCGA TCGGAGCCA GCGGCGCGG TACCCACAAC GGCUGGCTCG	180
CGCGCGTGA CGGCTGAGC GCCACCGCA CCGGCGACAC CTGTTGCCCC CGCAGCAGCG	240
GGCGCGGCGA ACACGCGGAA TGCGAGCGG GCGATCCCA AGCAGCGACC TCGCGCGGCG	300
GACCGGAAGC CACGCGCGGC ACCTGTCATT GCGCGAAGC CACCGGAGC TGTGCGGATC	360
GACAACCGCG TTGAGGATT CAGCTTGCG CTGCTGCTG GCTGCGTGA GTCTGAGCGC	420
GCGCACTTCG ACTAGGTTG AGCACTCTC AGCAAAACCA CCGGGGAGCC GGCATTTCCC	480
GGACAGCGCG CGCGGTTGTC CAATGACAC CTTATCGTGC TCGGCGGCT AGACCAAAAG	540
CTTACGCGCA GCGCGAAGC CACCGACTCC AAGCGCGCG GCGGTTGGG CTGCGACATG	600
GGTGAGTTCT ATATGCGCTA CCGGGGAGC CGGATCAACC AGGAAACGCT CTCGCTCGAC	660

```

GCCAACGGGG TGTCTGGGAG CGCCTCGTAT TACGAAGTCA AGTTCAGCGA TCCGAGTAAG      720
CCGAACGGCC AGATCTGGAC GGGCGTAATC GGCCTGCCCC CGGCGGACCC ACCGGACGCC      780
GGGCCCCCTC AGGCGCTGCT TGTGGTATGG CTGCGGACCG CCACACACCC GGTGGACAG      840
GGGCGGGCCA AGGCGCTGGC CCAATCGATC CGGCTTTTGG TGGCCCCGCC GCGGGCGCG      900
GCACCGGCTC CTGACAGAGC CGCTCCGGCG CCGGCGCTGG CCGGGGAAGT CGCTCTACC      960
CCGACGACAC CGACACCGCA GCGGACCTTA CCGGCTGA      999

```

(2) INFORMATION FOR SEQ ID NO:53:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1           5           10           15

Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20           25           30

Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35           40           45

Gln Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50           55           60

Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65           70           75           80

Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85           90           95

Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
100          105          110

Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
115          120          125

Phe Ala Leu Pro Ala Gly Trp Val Gln Ser Asp Ala Ala His Phe Asp
130          135          140

Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro

```

```

145              150              155              160
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
              165              170              175
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
              180              185              190
Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
              195              200              205
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
              210              215              220
Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
225              230              235              240
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
              245              250              255
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
              260              265              270
Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
              275              280              285
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
290              295              300
Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
305              310              315              320
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
              325              330

```

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Xaa Asn Tyr Gly Glu Val
1           5           10           15
Val Ala Ala Leu
              20

```

(2) INFORMATION FOR SEQ ID NO:55:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:56:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala	Ala	Lys
1			5					10							15

Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:57:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	Phe	Asp	Pro	Ala	Trp	Gly	Pro
1			5					10						15

(2) INFORMATION FOR SEQ ID NO:58:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Gln Gln Ser Ile Ser Thr Xaa Gln Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Gln Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO:61:

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(*i) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

Thr Gly Ser Leu Asn Glu Thr His Asn Arg Arg Ala Asn Glu Arg Lys
1           5           10           15

Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala
20           25           30

Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala
35           40           45

Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro
50           55           60

Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln
65           70           75           80

Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala
85           90           95

Asn Lys Gly Ser Leu Val Gln Gly Gly Ile Gly Gly Thr Gln Ala Arg
100          105          110

Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro
115          120          125

Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala
130          135          140

Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr
145          150          155          160

Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala
165          170          175

Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Xaa
180          185

```

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
1           5           10           15

Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser
          20           25           30

Gly Val Gln Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg
          35           40           45

Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser
          50           55           60

Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val
          65           70           75           80

Ser Arg Arg His Ala Glu Phe Arg Leu Gln Asn Asn Glu Phe Asn Val
          85           90           95

Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val
          100          105          110

Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu
          115          120          125

Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser
          130          135          140

Thr Gly Gly Pro
          145

```

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 230 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr
1           5           10           15

```

100

```

Gly Pro Asp Arg Ser Ala Ser Leu Ser Leu Val Arg His Arg Arg Gln
    20                      25                      30

Gln Arg Asp Ala Leu Cys Leu Ser Ser Thr Gln Ile Ser Arg Gln Ser
    35                      40                      45

Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn
    50                      55                      60

Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu
    65                      70                      75                      80

Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Glu
    85                      90                      95

Gln Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser
   100                      105                      110

Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp
   115                      120                      125

Gln Lys Ser Leu Gln Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu
   130                      135                      140

Ser Ala Ala Thr Ser Ser Thr Pro Arg Gln Ala Pro Tyr Gln Leu Asn
   145                      150                      155                      160

Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln
   165                      170                      175

Ala Val Val Leu Asn Val Tyr His Asn Ala Gly Gly Thr His Pro Thr
   180                      185                      190

Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile
   195                      200                      205

Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val
   210                      215                      220

Phe Pro Ile Val Ala Arg
   225                      230

```

(2) INFORMATION FOR SEQ ID NO:67:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1           5           10           15

Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20           25           30

Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35           40           45

Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50           55           60

Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65           70           75           80

Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85           90           95

Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100          105          110

Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115          120          125

Gly Pro Pro Ala
130

```

(xii) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
1           5           10           15

Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Arg Leu Ser Asn Pro Pro
20           25           30

Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
35           40           45

Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa
50           55           60

```

102

```

Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
65              70              75              80

Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
      85              90              95

Ser Glu Arg Lys
      100

```

(2) INFORMATION FOR SEQ ID NO:69:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(a) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
1              5              10              15

Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
      20              25              30

Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp
      35              40              45

Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
      50              55              60

Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu
      65              70              75              80

Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Gln Arg
      85              90              95

Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro
      100             105             110

Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
      115             120             125

Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg
      130             135             140

His Arg Xaa Gly Pro Val Asp Gln Pro Asp Arg Arg Leu Pro Val Arg
      145             150             155             160

Asp Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:70:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly
 1             5             10             15

Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg
      20             25             30

Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr
      35             40             45

Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Gln Val Pro
      50             55             60

Arg Gly Arg Lys Glu Ala Val Ala Ala Ala Val Ala Ala Ser Leu Arg
      65             70             75             80

Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly
      85             90             95

Gln Thr Asp Thr Ala Ala Ala Ile Leu Ala Gly Thr Ala Pro Ala Ala
      100            105            110

Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr
      115            120            125

Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Glu Tyr
      130            135            140

Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val
      145            150            155            160

Leu Leu Asp Gln Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu
      165            170            175

Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu
      180            185            190

His Arg Pro Gly Arg Ser Thr Arg Arg Leu Gln Pro Arg Thr Leu Pro
      195            200            205

Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe

```

104

210	215	220
Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro		
225	230	235 240
Thr Arg Glu Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro		
	245	250 255
Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro		
	260	265 270
Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala		
	275	280 285
Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu		
	290	295 300
Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr		
	305	310 315 320
Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Gln Gly Gln		
	325	330 335
Val Ser Arg Gln Asn Pro Thr Gly		
	340	

(2) INFORMATION FOR SEQ ID NO:71:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala	
1	5 10 15
Leu Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Gln Asp Cys Val Glu	
	20 25 30
Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile	
	35 40 45
Ile Tyr Arg Gln Arg Arg Ala Gln Leu Arg Thr Ala Lys Ala Leu Leu	
	50 55 60
Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Ala Val Thr Val Leu	
	65 70 75 80

Arg	Glu	Arg	Tyr	Leu	Leu	His	Asp	Gln	Gln	Gly	Arg	Pro	Ala	Glu	Ser		
				85					90					95			
Thr	Gly	Gln	Leu	Met	Asp	Arg	Ser	Ala	Arg	Cys	Val	Ala	Ala	Ala	Glu		
			100					105					110				
Asp	Gln	Tyr	Gln	Pro	Gly	Ser	Ser	Arg	Arg	Trp	Ala	Glu	Arg	Phe	Ala		
		115					120					125					
Thr	Leu	Leu	Arg	Asn	Leu	Glu	Phe	Leu	Pro	Asn	Ser	Pro	Thr	Leu	Met		
	130				135						140						
Asn	Ser	Gly	Thr	Asp	Leu	Gly	Leu	Leu	Ala	Gly	Cys	Phe	Val	Leu	Pro		
145					150					155					160		
Ile	Gln	Asp	Ser	Leu	Gln	Ser	Ile	Phe	Ala	Thr	Leu	Gly	Gln	Ala	Ala		
			165						170					175			
Glu	Leu	Gln	Arg	Ala	Gly	Gly	Gly	Thr	Gly	Tyr	Ala	Phe	Ser	His	Leu		
			180					185					190				
Arg	Pro	Ala	Gly	Asp	Arg	Val	Ala	Ser	Thr	Gly	Gly	Thr	Ala	Ser	Gly		
		195					200					205					
Pro	Val	Ser	Phe	Leu	Arg	Leu	Tyr	Asp	Ser	Ala	Ala	Gly	Val	Val	Ser		
	210					215					220						
Met	Gly	Gly	Arg	Arg	Arg	Gly	Ala	Cys	Met	Ala	Val	Leu	Asp	Val	Ser		
225					230					235					240		
His	Pro	Asp	Ile	Cys	Asp	Phe	Val	Thr	Ala	Lys	Ala	Glu	Ser	Pro	Ser		
			245						250					255			
Glu	Leu	Pro	His	Phe	Asn	Leu	Ser	Val	Gly	Val	Thr	Asp	Ala	Phe	Leu		
		260						265					270				
Arg	Ala	Val	Glu	Arg	Asn	Gly	Leu	His	Arg	Leu	Val	Asn	Pro	Arg	Thr		
		275				280						285					
Gly	Lys	Ile	Val	Ala	Arg	Met	Pro	Ala	Ala	Glu	Leu	Phe	Asp	Ala	Ile		
	290					295					300						
Cys	Lys	Ala	Ala	His	Ala	Gly	Gly	Asp	Pro	Gly	Leu	Val	Phe	Leu	Asp		
305					310					315					320		
Thr	Ile	Asn	Arg	Ala	Asn	Pro	Val	Pro	Gly	Arg	Gly	Arg	Ile	Glu	Ala		
			325						330					335			
Thr	Asn	Pro	Cys	Gly	Glu	Val	Pro	Leu	Leu	Pro	Tyr	Glu	Ser	Cys	Asn		
		340					345						350				
Leu	Gly	Ser	Ile	Asn	Leu	Ala	Arg	Met	Leu	Ala	Asp	Gly	Arg	Val	Asp		
	355					360					365						
Trp	Asp	Arg	Leu	Glu	Glu	Val	Ala	Gly	Val	Ala	Val	Arg	Phe	Leu	Asp		

```

          370          375          380
Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala
385          390          395          400

Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu
          405          410          415

Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg
          420          425          430

Leu Ala Thr Arg Leu Met Arg Arg Ile Gln Gln Ala Ala His Thr Ala
          435          440          445

Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp
          450          455          460

Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser
          465          470          475          480

Val Ala Pro Thr Gly
          485

```

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 287 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Gly Val Ile Val Leu Asp Leu Gln Pro Arg Gly Pro Leu Pro Thr Glu
1           5           10           15

Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val
20          25          30

Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala
35          40          45

Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His
50          55          60

Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu
65          70          75          80

Gly Asn Ala Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Gln Thr Pro
85          90          95

```


107

```

Thr Pro Thr Ala Ala Val Gln Pro Pro Pro Val Leu Lys Glu Gly Asp
      100                      105                      110

Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro
      115                      120                      125

Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn
      130                      135                      140

Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala
      145                      150                      155                      160

Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp
      165                      170                      175

Cys Ala Pro Ser Asn Glu Thr Leu Val Lys Thr Phe Ser Pro Gly Glu
      180                      185                      190

Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg
      195                      200                      205

Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val
      210                      215                      220

Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn
      225                      230                      235                      240

Gln Pro Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln
      245                      250                      255

Ala Pro Pro Pro Glu Ser Pro Ala Gln Gly Gly
      260                      265

```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val
1           5           10           15

Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala
      20           25           30

Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr
      35           40           45

```

108

```

Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala
 50                      55                      60

Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp
 65                      70                      75                      80

Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Glu
      85                      90                      95

Gln

```

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 364 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala
1           5           10           15

Cys Gly Gly Gly Thr Asn Ser Ser Ser Ser Gly Ala Gly Gly Thr Ser
      20           25           30

Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser
      35           40           45

Thr Ala Gln Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg
      50           55           60

Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala
      65           70           75           80

Gly Val Thr Gln Phe Leu Asn Asn Glu Thr Asp Phe Ala Gly Ser Asp
      85           90           95

Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Glu Arg
      100          105          110

Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro Ile Ala
      115          120          125

Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro
      130          135          140

Thr Thr Ala Lys Ile Phe Asn Gly Thr Ile Thr Val Trp Asn Asp Pro

```

109

145		150		155		160
Gln Ile Gln Ala Leu Asn Ser Gly Thr Asp Leu Pro Pro Thr Pro Ile						
	165			170		175
Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln						
	180		185			190
Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser						
	195	200			205	
Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly						
	210	215		220		
Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Gln						
	225	230		235		240
Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr						
	245		250			255
Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys						
	260		265			270
Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu						
	275	280		285		
Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile						
	290	295		300		
Val Leu Ala Thr Tyr Gln Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr						
	305	310		315		320
Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly						
	325		330			335
Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe						
	340		345			350
Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser						
	355	360				

(2) INFORMATION FOR SEQ ID NO:75:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Asp
 1 5 10 15
 Gln Thr His Glu Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val
 20 25 30
 Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro
 35 40 45
 Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser
 50 55 60
 Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg
 65 70 75 80
 Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro
 85 90 95
 Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg
 100 105 110
 Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp
 115 120 125
 Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val
 130 135 140
 Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg
 145 150 155 160
 Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly
 165 170 175
 Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala
 180 185 190
 Ala Val Glu Asp Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val
 195 200 205
 Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg
 210 215 220
 Ala Gly Pro Glu Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro
 225 230 235 240
 Leu Pro Ala Arg Ala Gly Gln Gln Gln Pro Ser Ser Ala Gly Gly Arg
 245 250 255
 Arg Ala Gly Gly Ala Gln Arg Ala Asp Pro Gly Gln Arg Gly Arg His
 260 265 270
 His Gln Gly Gly His Asp Pro Gly Arg Gln Gly Ala Gln Arg Gly Thr
 275 280 285
 Ala Gly Val Ala His Ala Ala Ala Gly Pro Arg Arg Ala Ala Val Arg

Gly	Leu	Ile	Pro	Gly	Val	Ile	Pro	Thr	Met	Thr	Pro	Pro	Pro	Gly	Met
	195						200					205			
Val	Arg	Gln	Arg	Pro	Arg	Ala	Gly	Met	Leu	Ala	Ile	Gly	Ala	Val	Thr
	210					215					220				
Ile	Ala	Val	Val	Ser	Ala	Gly	Ile	Gly	Gly	Ala	Ala	Ala	Ser	Leu	Val
225					230					235				240	
Gly	Phe	Asn	Arg	Ala	Pro	Ala	Gly	Pro	Ser	Gly	Gly	Pro	Val	Ala	Ala
				245					250					255	
Ser	Ala	Ala	Pro	Ser	Ile	Pro	Ala	Ala	Asn	Met	Pro	Pro	Gly	Ser	Val
			260					265					270		
Glu	Gln	Val	Ala	Ala	Lys	Val	Val	Pro	Ser	Val	Val	Met	Leu	Glu	Thr
	275					280						285			
Asp	Leu	Gly	Arg	Gln	Ser	Glu	Gln	Gly	Ser	Gly	Ile	Ile	Leu	Ser	Ala
290						295					300				
Glu	Gly	Leu	Ile	Leu	Thr	Asn	Asn	His	Val	Ile	Ala	Ala	Ala	Ala	Lys
305					310					315					320
Pro	Pro	Leu	Gly	Ser	Pro	Pro	Pro	Lys	Thr	Thr	Val	Thr	Phe	Ser	Asp
			325						330					335	
Gly	Arg	Thr	Ala	Pro	Phe	Thr	Val	Val	Gly	Ala	Asp	Pro	Thr	Ser	Asp
			340					345					350		
Ile	Ala	Val	Val	Arg	Val	Gln	Gly	Val	Ser	Gly	Leu	Thr	Pro	Ile	Ser
	355					360						365			
Leu	Gly	Ser	Ser	Ser	Asp	Leu	Arg	Val	Gly	Gln	Pro	Val	Leu	Ala	Ile
	370					375					380				
Gly	Ser	Pro	Leu	Gly	Leu	Gln	Gly	Thr	Val	Thr	Thr	Gly	Ile	Val	Ser
385					390					395				400	
Ala	Leu	Asn	Arg	Pro	Val	Ser	Thr	Thr	Gly	Gln	Ala	Gly	Asn	Gln	Asn
				405					410					415	
Thr	Val	Leu	Asp	Ala	Ile	Gln	Thr	Asp	Ala	Ala	Ile	Asn	Pro	Gly	Asn
			420					425					430		
Ser	Gly	Gly	Ala	Leu	Val	Asn	Met	Asn	Ala	Gln	Leu	Val	Gly	Val	Asn
	435						440					445			
Ser	Ala	Ile	Ala	Thr	Leu	Gly	Ala	Asp	Ser	Ala	Asp	Ala	Gln	Ser	Gly
	450					455					460				
Ser	Ile	Gly	Leu	Gly	Phe	Ala	Ile	Pro	Val	Asp	Gln	Ala	Lys	Arg	Ile
465					470					475					480
Ala	Asp	Gln	Leu	Ile	Ser	Thr	Gly	Lys	Ala	Ser	Sis	Ala	Ser	Leu	Gly

485										490					495				
Val	Gln	Val	Thr	Asn	Asp	Lys	Asp	Thr	Pro	Gly	Ala	Lys	Ile	Val	Glu				
500								505				510							
Val	Val	Ala	Gly	Gly	Ala	Ala	Ala	Asn	Ala	Gly	Val	Pro	Lys	Gly	Val				
515								520				525							
Val	Val	Thr	Lys	Val	Asp	Asp	Arg	Pro	Ile	Asn	Ser	Ala	Asp	Ala	Leu				
530								535				540							
Val	Ala	Ala	Val	Arg	Ser	Lys	Ala	Pro	Gly	Ala	Thr	Val	Ala	Leu	Thr				
545								550				555				560			
Phe	Gln	Asp	Pro	Ser	Gly	Gly	Ser	Arg	Thr	Val	Gln	Val	Thr	Leu	Gly				
				565				570								575			
Lys	Ala	Gln	Gln																
580																			

(2) INFORMATION FOR SEQ ID NO: 77:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(4) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Met	Asp	Asp	Gly	Lys	Arg	Ala	Val	Thr	Ser	Ala	Val	Leu	Val	Val	Leu
1				5					10					15	
Gly	Ala	Cys	Leu	Ala	Leu	Trp	Leu	Ser	Gly	Cys	Ser	Ser	Pro	Lys	Pro
			20					25					30		
Asp	Ala	Glu	Gln	Glu	Gly	Val	Pro	Val	Ser	Pro	Thr	Ala	Ser	Asp	Pro
			35				40					45			
Ala	Leu	Leu	Ala	Gln	Ile	Arg	Gln	Ser	Leu	Asp	Ala	Thr	Lys	Gly	Leu
	50					55					60				
Thr	Ser	Val	Sis	Val	Ala	Val	Arg	Thr	Thr	Gly	Lys	Val	Asp	Ser	Leu
65					70					75					80
Leu	Gly	Ile	Thr	Ser	Ala	Asp	Val	Asp	Val	Arg	Ala	Asn	Pro	Leu	Ala
				85					90					95	
Ala	Lys	Gly	Val	Cys	Thr	Tyr	Asn	Asp	Glu	Gln	Gly	Val	Pro	Phe	Arg
			100					105					110		

114

```

Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp Asp Trp Ser Asn
    115                      120                      125

Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val Leu Asp Pro Ala
    130                      135                      140

Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn Leu Gln Ala Gln
    145                      150                      155                      160

Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys Ile Thr Gly Thr
    165                      170                      175

Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly Ala Lys Ser Ala
    180                      185                      190

Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser His His Leu Val
    195                      200                      205

Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln Leu Thr Gln Ser
    210                      215                      220

Lys Trp Asp Glu Pro Val Asn Val Asp
    225                      230

```

(2) INFORMATION FOR SEQ ID NO:76:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala
1           5           10           15

Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
20           25           30

Ala Arg Val Ile Gln Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
35           40           45

Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
50           55           60

Pro Arg
65

```

(2) INFORMATION FOR SEQ ID NO:75:

115

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

Val Pro Pro Ala Pro Pro Leu Pro Pro Leu Pro Pro Ser Pro Ile Ser
1           5           10           15

Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
          20           25           30

Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro
35           40           45

Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
50           55           60

Ser Pro Pro Leu Pro
65

```

(2) INFORMATION FOR SEQ ID NO:80:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
1           5           10           15

Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
          20           25           30

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
35           40           45

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
50           55           60

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
65           70           75           80

```

116

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Gln Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Gln Gln Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Gln Gly
 340 345 350
 Pro Pro Ala
 355

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```

Ser Pro Lys Pro Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr
1           5           10           15

Ala Ser Asp Pro Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala
20           25           30

Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys
35           40           45

Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala
50           55           60

Asn Pro Leu Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Gln Gln Gly
65           70           75           80

Val Pro Phe Arg Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp
85           90           95

Asp Trp Ser Asn Leu Gly Ser Ile Ser Gln Leu Ser Thr Ser Arg Val
100          105          110

Leu Asp Pro Ala Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn
115          120          125

Leu Gln Ala Gln Gly Thr Gln Val Ile Asp Gly Ile Ser Thr Thr Lys
130          135          140

Ile Thr Gly Thr Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly
145          150          155          160

Ala Lys Ser Ala Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser
165          170          175

His His Leu Val Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln
180          185          190

Leu Thr Gln Ser Lys Trp Asn Gln Pro Val Asn Val Asp
195          200          205

```

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Gly	Asp	Ser	Phe	Trp	Ala	Ala	Ala	Asp	Gln	Met	Ala	Arg	Gly	Phe	Val	1	5	10	15
Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Leu	Thr	Gly	Glu	Gly	Leu	Gln	20	25	30	
His	Ala	Asp	Gly	His	Ser	Leu	Leu	Leu	Asp	Ala	Thr	Asn	Pro	Ala	Val	35	40	45	
Val	Ala	Tyr	Asp	Pro	Ala	Phe	Ala	Tyr	Glu	Ile	Gly	Tyr	Ile	Xaa	Glu	50	55	60	
Ser	Gly	Leu	Ala	Arg	Met	Cys	Gly	Glu	Asn	Pro	Glu	Asn	Ile	Phe	Phe	65	70	75	80
Tyr	Ile	Thr	Val	Tyr	Asn	Glu	Pro	Tyr	Val	Gln	Pro	Pro	Glu	Pro	Glu	85	90	95	
Asn	Phe	Asp	Pro	Glu	Gly	Val	Leu	Gly	Gly	Ile	Tyr	Arg	Tyr	His	Ala	100	105	110	
Ala	Thr	Glu	Gln	Arg	Thr	Asn	Lys	Xaa	Gln	Ile	Leu	Ala	Ser	Gly	Val	115	120	125	
Ala	Met	Pro	Ala	Ala	Leu	Arg	Ala	Ala	Gln	Met	Leu	Ala	Ala	Glu	Trp	130	135	140	
Asp	Val	Ala	Ala	Asp	Val	Trp	Ser	Val	Thr	Ser	Trp	Gly	Glu	Leu	Asn	145	150	155	160
Arg	Asp	Gly	Val	Val	Ile	Gln	Thr	Glu	Lys	Leu	Arg	His	Pro	Asp	Arg	165	170	175	
Pro	Ala	Gly	Val	Pro	Tyr	Val	Thr	Arg	Ala	Leu	Glu	Asn	Ala	Arg	Gly	180	185	190	
Pro	Val	Ile	Ala	Val	Ser	Asp	Trp	Met	Arg	Ala	Val	Pro	Glu	Gln	Ile	195	200	205	
Arg	Pro	Trp	Val	Pro	Gly	Thr	Tyr	Leu	Thr	Leu	Gly	Thr	Asp	Gly	Phe	210	215	220	
Gly	Phe	Ser	Asp	Thr	Arg	Pro	Ala	Gly	Arg	Arg	Tyr	Phe	Asn	Thr	Asp				

225		230		235		240									
Ala	Glu	Ser	Gln	Val	Gly	Arg	Gly	Phe	Gly	Arg	Gly	Trp	Pro	Gly	Arg
				245					250					255	
Arg	Val	Asn	Ile	Asp	Pro	Phe	Gly	Ala	Gly	Arg	Gly	Pro	Pro	Ala	Gln
				260				265					270		
Leu	Pro	Gly	Phe	Asp	Glu	Gly	Gly	Gly	Leu	Arg	Pro	Asa	Lys		
		275					280					285			

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Thr	Lys	Phe	His	Ala	Leu	Met	Gln	Glu	Gln	Ile	His	Asn	Glu	Phe	Thr
1				5						10				15	
Ala	Ala	Gln	Gln	Tyr	Val	Ala	Ile	Ala	Val	Tyr	Phe	Asp	Ser	Glu	Asp
			20					25					30		
Leu	Pro	Gln	Leu	Ala	Lys	His	Phe	Tyr	Ser	Gln	Ala	Val	Glu	Glu	Arg
		35					40					45			
Asn	His	Ala	Met	Met	Leu	Val	Gln	His	Leu	Leu	Asp	Arg	Asp	Leu	Arg
		50				55					60				
Val	Glu	Ile	Pro	Gly	Val	Asp	Thr	Val	Arg	Asn	Glu	Phe	Asp	Arg	Pro
65					70					75				80	
Arg	Gln	Ala	Leu	Ala	Leu	Ala	Leu	Asp	Gln	Glu	Arg	Thr	Val	Thr	Asp
			85					90						95	
Gln	Val	Gly	Arg	Leu	Thr	Ala	Val	Ala	Arg	Asp	Glu	Gly	Asp	Phe	Leu
			100					105					110		
Gly	Gln	Gln	Phe	Met	Gln	Trp	Phe	Leu	Gln	Glu	Gln	Ile	Gln	Gln	Val
		115				120						125			
Ala	Leu	Met	Ala	Thr	Leu	Val	Arg	Val	Ala	Asp	Arg	Ala	Gly	Ala	Asn
		130				135					140				
Leu	Phe	Glu	Leu	Glu	Asn	Phe	Val	Ala	Arg	Glu	Val	Asp	Val	Ala	Pro
145				150						155				160	

120

Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Arg Ala Asp Glu Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser Ile
 1 5 10 15

Ala Ala Gly Leu Thr Ala Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly
 20 25 30

Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro
 35 40 45

Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa
 50 55 60

Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp
 65 70 75 80

Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Glu Gly Gly Ile
 85 90 95

Gly Gly Xaa Glu Gly Xaa Xaa Arg Arg Xaa Gln
 100 105

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn
 1 5 10 15

Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr

121

	20		25		30
Arg Arg Ala Leu Glu Leu Gln Ala Pro Ser Val Val Xaa Arg Gln Gly	35		40		45
Val Lys Glu Pro Leu Xaa Thr Gly Ile Lys Ala Ile Asp Ala Met Thr	50		55		60
Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr	65		70		75
Gly Lys Asn Arg Arg Leu Cys Arg Thr Pro Ser Ser Asn Gln Arg Glu	85		90		95
Gln Leu Gly Val Arg Trp Ile Pro Arg Ser Arg Cys Ala Cys Val Tyr	100		105		110
Val Gly His Arg Ala Arg Arg Gly Thr Tyr His Arg Arg	115		120		125

(2) INFORMATION FOR SEQ ID NO:86:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(a1) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Cys Asp Ala Val Met Gly Phe Leu Gly Gly Ala Gly Pro Leu Ala Val	1	5	10	15
Val Asp Gln Gln Leu Val Thr Arg Val Pro Gln Gly Trp Ser Phe Ala	20	25	30	
Gln Ala Ala Ala Val Pro Val Val Phe Leu Thr Ala Trp Tyr Gly Leu	35	40	45	
Ala Asp Leu Ala Gln Ile Lys Ala Gly Glu Ser Val Leu Ile His Ala	50	55	60	
Gly Thr Gly Gly Val Gly Met Ala Ala Val Gln Leu Ala Arg Gln Trp	65	70	75	80
Gly Val Glu Val Phe Val Thr Ala Ser Arg Gly Lys Trp Asp Thr Leu	85	90	95	
Arg Ala Xaa Xaa Phe Asp Asp Xaa Pro Tyr Arg Xaa Phe Pro His Xaa	100	105	110	

122

Arg Ser Ser Xaa Gly
115

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met	Tyr	Arg	Phe	Ala	Cys	Arg	Thr	Leu	Met	Leu	Ala	Ala	Cys	Ile	Leu
1				5				10						15	
Ala	Thr	Gly	Val	Ala	Gly	Leu	Gly	Val	Gly	Ala	Gln	Ser	Ala	Ala	Gln
			20				25						30		
Thr	Ala	Pro	Val	Pro	Asp	Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	Phe	Asp
		35				40						45			
Pro	Ala	Trp	Gly	Pro	Asn	Trp	Asp	Pro	Tyr	Thr	Cys	His	Asp	Asp	Phe
		50				55					60				
His	Arg	Asp	Ser	Asp	Gly	Pro	Asp	His	Ser	Arg	Asp	Tyr	Pro	Gly	Pro
65					70					75				80	
Ile	Leu	Glu	Gly	Pro	Val	Leu	Asp	Asp	Pro	Gly	Ala	Ala	Pro	Pro	Pro
			85					90						95	
Pro	Ala	Ala	Gly	Gly	Gly	Ala									
						100									

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Val	Gln	Cys	Arg	Val	Trp	Leu	Gln	Ile	Gln	Trp	Arg	Gly	Met	Leu	Gly
1				5				10						15	

123

```

Ala Asp Gln Ala Arg Ala Gly Gly Pro Ala Arg Ile Trp Arg Glu His
  20                      25                      30

Ser Met Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala
  35                      40                      45

Thr Lys Glu Gly Arg Gly Ile Val Met Arg Val Pro Leu Glu Gly Gly
  50                      55                      60

Gly Arg Leu Val Val Glu Leu Thr Pro Asp Glu Ala Ala Ala Leu Gly
  65                      70                      75                      80

Asp Glu Leu Lys Gly Val Thr Ser
  85

```

(2) INFORMATION FOR SEQ ID NO:89:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
  1                      5                      10                      15

Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
  20                      25                      30

Ser Leu Glu Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
  35                      40                      45

Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
  50                      55                      60

Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
  65                      70                      75                      80

Ala Asp Glu Glu Gln Gln Glu Ala Leu Ser Ser Gln Met Gly Phe
  85                      90                      95

```

(2) INFORMATION FOR SEQ ID NO:90:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met	Thr	Gln	Ser	Gln	Thr	Val	Thr	Val	Asp	Gln	Gln	Glu	Ile	Leu	Asn	1	5	10	15
Arg	Ala	Asn	Glu	Val	Glu	Ala	Pro	Met	Ala	Asp	Pro	Pro	Thr	Asp	Val	20	25	30	
Pro	Ile	Thr	Pro	Cys	Glu	Leu	Thr	Xaa	Xaa	Lys	Asn	Ala	Ala	Gln	Gln	35	40	45	
Xaa	Val	Leu	Ser	Ala	Asp	Asn	Met	Arg	Glu	Tyr	Leu	Ala	Ala	Gly	Ala	50	55	60	
Lys	Glu	Arg	Gln	Arg	Leu	Ala	Thr	Ser	Leu	Arg	Asn	Ala	Ala	Lys	Xaa	65	70	75	80
Tyr	Gly	Glu	Val	Asp	Glu	Glu	Ala	Ala	Thr	Ala	Leu	Asp	Asn	Asp	Gly	85	90	95	
Glu	Gly	Thr	Val	Gln	Ala	Glu	Ser	Ala	Gly	Ala	Val	Gly	Gly	Asp	Ser	100	105	110	
Ser	Ala	Glu	Leu	Thr	Asp	Thr	Pro	Arg	Val	Ala	Thr	Ala	Gly	Glu	Pro	115	120	125	
Asn	Phe	Met	Asp	Leu	Lys	Glu	Ala	Ala	Arg	Lys	Leu	Glu	Thr	Gly	Asp	130	135	140	
Gln	Gly	Ala	Ser	Leu	Ala	His	Xaa	Gly	Asp	Gly	Tyr	Asn	Thr	Xaa	Thr	145	150	155	160
Leu	Thr	Leu	Gln	Gly	Asp											165			

(2) INFORMATION FOR SEQ ID NO:91:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Arg	Ala	Glu	Arg	Met
1				5

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

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Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
1           5           10           15

Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
20           25           30

Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
35           40           45

Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
50           55           60

Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
65           70           75           80

Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
85           90           95

Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
100          105          110

Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asp Gln Leu Met
115          120          125

Asn Asn Val Pro Gln Ala Leu Lys Glu Leu Ala Glu Pro Thr Gln Gly
130          135          140

Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
145          150          155          160

His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
165          170          175

Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
180          185          190

Leu Lys Gly Phe Ala Pro Ala Ala Ala Glu Ala Val Gln Thr Ala
195          200          205

Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly

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210	215	220
Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala		
225	230	235 240
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly		
	245 250	255
Arg Arg Asn Gly Gly Pro Ala		
	260	

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala		
1	5	10 15
Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly		
	20 25	30
Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly		
	35 40	45
Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr		
	50 55	60
Gln Leu Gly Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro		
	65 70	75 80
Val Gly Val Ala Leu Leu Ala Ala Leu Leu Ala Gly Val Val Leu Val		
	85 90	95
Pro Lys Ala Lys Ser His Val Thr Val Val Ala Val Leu Gly Val Leu		
	100 105	110
Gly Val Phe Leu Met Val Ser Ala Thr Phe Asn Lys Pro Ser Ala Tyr		
	115 120	125
Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln		
	130 135	140
Ala Val Ala Ala Val Leu Ala Leu Leu Val Glu Thr Gly Ala Ile Thr		
	145 150	155 160

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Ala	Pro	Ala	Pro	Arg	Pro	Lys	Phe	Asp	Pro	Tyr	Gly	Gln	Tyr	Gly	Arg
				165					170					175	
Tyr	Gly	Gln	Tyr	Gly	Gln	Tyr	Gly	Val	Gln	Pro	Gly	Gly	Tyr	Tyr	Gly
		180						185					190		
Gln	Gln	Gly	Ala	Gln	Gln	Ala	Ala	Gly	Leu	Gln	Ser	Pro	Gly	Pro	Gln
		195					200					205			
Gln	Ser	Pro	Gln	Pro	Pro	Gly	Tyr	Gly	Ser	Gln	Tyr	Gly	Gly	Tyr	Ser
	210					215					220				
Ser	Ser	Pro	Ser	Gln	Ser	Gly	Ser	Gly	Tyr	Thr	Ala	Gln	Pro	Pro	Ala
225					230					235					240
Gln	Pro	Pro	Ala	Gln	Ser	Gly	Ser	Gln	Gln	Ser	Sis	Gln	Gly	Pro	Ser
			245					250					255		
Thr	Pro	Pro	Thr	Gly	Phe	Pro	Ser	Phe	Ser	Pro	Pro	Pro	Pro	Val	Ser
			260					265						270	
Ala	Gly	Thr	Gly	Ser	Gln	Ala	Gly	Ser	Ala	Pro	Val	Asn	Tyr	Ser	Asn
	275						280					285			
Pro	Ser	Gly	Gly	Gln	Gln	Ser	Ser	Ser	Pro	Gly	Gly	Ala	Pro	Val	
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 507 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGAAGATGG	TGAAATCCAT	CGCCGCAGGT	CTCACCGCCG	CGGCTGCAAT	CGGCSCCGCT	60
GCGGCGCGTC	TGACTTCGAT	CATGGCTGAC	GGCCCGGTCG	TATACAGAT	GCAGCCGCTC	120
GTCTTCGGGG	CGCCACTGCC	GTGGACCCG	GCATCCGCCC	CTGACGTCCC	GACCGCCGCC	180
CAGTTGACCA	GCTGCTCAA	CAGCTCCGCC	GATCCCAAGC	TCTCGTTTCC	GAACAAGGGC	240
AGTCTGCTCG	AGGCGGGCAT	CGGGGCGACC	GAGGCGGCGA	TGGCGGACCA	CAAGCTGAAG	300
AAAGCCGCGG	AGCACGGGGA	TCTGCGGCTG	TGTTTCAGCG	TGACGAACAT	CCAGCCGCGG	360
GCGGCGGGTT	CGGCCACCGC	CGACGTTTCC	GTCTCGGGTC	CGAAGCTCTC	GTGCGCGGTC	420

ACGCAGACG TGCCTTCGT GATCAGGCG GCGTCGATGC TGTACGCGC ATCGGCGATG 480
 GAGTTGCTCG AGGCGCGAGG GAACTGA 507

(2) INFORMATION FOR SEQ ID NO:95:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met	Lys	Met	Val	Lys	Ser	Ile	Ala	Ala	Gly	Leu	Thr	Ala	Ala	Ala	Ala	1	5	10	15
Ile	Gly	Ala	Ala	Ala	Ala	Gly	Val	Thr	Ser	Ile	Met	Ala	Gly	Gly	Pro	20	25	30	
Val	Val	Tyr	Gln	Met	Gln	Pro	Val	Val	Phe	Gly	Ala	Pro	Leu	Pro	Leu	35	40	45	
Asp	Pro	Ala	Ser	Ala	Pro	Asp	Val	Pro	Thr	Ala	Ala	Gln	Leu	Thr	Ser	50	55	60	
Leu	Leu	Asn	Ser	Leu	Ala	Asp	Pro	Asn	Val	Ser	Phe	Ala	Asn	Lys	Gly	65	70	75	80
Ser	Leu	Val	Gln	Gly	Gly	Ile	Gly	Gly	Thr	Gln	Ala	Arg	Ile	Ala	Asp	85	90	95	
His	Lys	Leu	Lys	Lys	Ala	Ala	Gln	His	Gly	Asp	Leu	Pro	Leu	Ser	Phe	100	105	110	
Ser	Val	Thr	Asn	Ile	Gln	Pro	Ala	Ala	Ala	Gly	Ser	Ala	Thr	Ala	Asp	115	120	125	
Val	Ser	Val	Ser	Gly	Pro	Lys	Leu	Ser	Ser	Pro	Val	Thr	Gln	Asn	Val	130	135	140	
Thr	Phe	Val	Asn	Gln	Gly	Gly	Trp	Met	Leu	Ser	Arg	Ala	Ser	Ala	Met	145	150	155	160
Gln	Leu	Leu	Gln	Ala	Ala	Gly	Asn									165			

(2) INFORMATION FOR SEQ ID NO:96:

(1) SEQUENCE CHARACTERISTICS: